

09/232,280

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION  
International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

|                                                                                      |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                        |                           |
|--------------------------------------------------------------------------------------|--|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------|---------------------------|
| (51) International Patent Classification <sup>6</sup> :                              |  | A2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | (11) International Publication Number: | WO 98/37093               |
| C07K 14/00, A61K 39/00                                                               |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | (43) International Publication Date:   | 27 August 1998 (27.08.98) |
| (21) International Application Number:                                               |  | PCT/US98/03492                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                        |                           |
| (22) International Filing Date:                                                      |  | 25 February 1998 (25.02.98)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                        |                           |
| (30) Priority Data:                                                                  |  | (81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). |                                        |                           |
| (71) Applicant:                                                                      |  | CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                        |                           |
| (72) Inventors:                                                                      |  | XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US).                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                        |                           |
| (74) Agents:                                                                         |  | MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                        |                           |
| (54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                        |                           |
| (57) Abstract                                                                        |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                        |                           |

Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides.

**FOR THE PURPOSES OF INFORMATION ONLY**

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

|    |                          |    |                                          |    |                                              |    |                          |
|----|--------------------------|----|------------------------------------------|----|----------------------------------------------|----|--------------------------|
| AL | Albania                  | ES | Spain                                    | LS | Lesotho                                      | SI | Slovenia                 |
| AM | Armenia                  | FI | Finland                                  | LT | Lithuania                                    | SK | Slovakia                 |
| AT | Austria                  | FR | France                                   | LU | Luxembourg                                   | SN | Senegal                  |
| AU | Australia                | GA | Gabon                                    | LV | Latvia                                       | SZ | Swaziland                |
| AZ | Azerbaijan               | GB | United Kingdom                           | MC | Monaco                                       | TD | Chad                     |
| BA | Bosnia and Herzegovina   | GE | Georgia                                  | MD | Republic of Moldova                          | TG | Togo                     |
| BB | Barbados                 | GH | Ghana                                    | MG | Madagascar                                   | TJ | Tajikistan               |
| BE | Belgium                  | GN | Guinea                                   | MK | The former Yugoslav<br>Republic of Macedonia | TM | Turkmenistan             |
| BF | Burkina Faso             | GR | Greece                                   | ML | Mali                                         | TR | Turkey                   |
| BG | Bulgaria                 | HU | Hungary                                  | MN | Mongolia                                     | TT | Trinidad and Tobago      |
| BJ | Benin                    | IE | Ireland                                  | MR | Mauritania                                   | UA | Ukraine                  |
| BR | Brazil                   | IL | Israel                                   | MW | Malawi                                       | UG | Uganda                   |
| BY | Belarus                  | IS | Iceland                                  | MX | Mexico                                       | US | United States of America |
| CA | Canada                   | IT | Italy                                    | NE | Niger                                        | UZ | Uzbekistan               |
| CF | Central African Republic | JP | Japan                                    | NL | Netherlands                                  | VN | Viet Nam                 |
| CG | Congo                    | KE | Kenya                                    | NO | Norway                                       | YU | Yugoslavia               |
| CH | Switzerland              | KG | Kyrgyzstan                               | NZ | New Zealand                                  | ZW | Zimbabwe                 |
| CI | Côte d'Ivoire            | KP | Democratic People's<br>Republic of Korea | PL | Poland                                       |    |                          |
| CM | Cameroon                 | KR | Republic of Korea                        | PT | Portugal                                     |    |                          |
| CN | China                    | KZ | Kazakhstan                               | RO | Romania                                      |    |                          |
| CU | Cuba                     | LC | Saint Lucia                              | RU | Russian Federation                           |    |                          |
| CZ | Czech Republic           | LI | Liechtenstein                            | SD | Sudan                                        |    |                          |
| DE | Germany                  | LK | Sri Lanka                                | SE | Sweden                                       |    |                          |
| DK | Denmark                  | LR | Liberia                                  | SG | Singapore                                    |    |                          |
| EE | Estonia                  |    |                                          |    |                                              |    |                          |

## COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE

### TECHNICAL FIELD

The present invention relates generally to compositions and methods for the treatment of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein and to DNA molecules encoding such polypeptides. Such polypeptides may be used in vaccines and pharmaceutical compositions for treatment of prostate cancer.

### BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved vaccines and treatment methods for prostate cancer.

## SUMMARY OF THE INVENTION

The present invention provides compounds and methods for immunotherapy of prostate cancer. In one aspect, polypeptides are provided comprising at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants thereof.

In related aspects, DNA molecules encoding the above polypeptides are provided. In specific embodiments, such DNA molecules include sequences provided in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224. The present invention further provides expression vectors comprising the above DNA molecules and host cells transformed or transfected with such expression vectors. In preferred embodiments, the host cells are selected from the group consisting of *E. coli*, yeast and mammalian cells.

In another aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, an inventive polypeptide and a known prostate antigen.

The present invention also provides pharmaceutical compositions comprising one or more of the above polypeptides, or a DNA molecule encoding such polypeptides, and a physiologically acceptable carrier, together with vaccines comprising one or more of such polypeptide or DNA molecules in combination with a non-specific immune response enhancer.

In related aspects, pharmaceutical compositions for the treatment of prostate cancer comprising one or more polypeptides and a physiologically acceptable carrier are provided, wherein the polypeptide comprises an immunogenic portion of a prostate tumor protein or of a variant of said protein that differs only in conservative substitutions and/or modifications, the prostate tumor protein being encoded by a DNA molecule having a

sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants thereof. The invention also provides vaccines for the treatment of prostate cancer comprising such polypeptides in combination with a non-specific immune response enhancer, together with pharmaceutical compositions and vaccines comprising one or more DNA molecules having a sequence provided in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221. Pharmaceutical compositions and vaccines comprising one or more of the above fusion proteins are also provided.

In yet another aspect, methods are provided for inhibiting the development of prostate cancer in a patient, comprising administering an effective amount of at least one of the above pharmaceutical compositions and/or vaccines.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunotherapy of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant of such a protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-

65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 181, 188, 191, 193, 194, 198, 203, 204, and 207-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example,  $^{125}\text{I}$ -labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of

one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers

to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (or a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a

growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain preferred embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end

of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may generally be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the

immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or fusion proteins comprising one or more such polypeptides and/or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides (or fusion proteins or DNA molecules encoding such polypeptides) may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide or fusion protein is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (*e.g.*, polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (*i.e.*, a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the

use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (*i.e.*, untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 µg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary

depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE<sup>TM</sup> system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

Polypeptides of the present invention may also, or alternatively, be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of one or more of the

above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20<sup>TM</sup> (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20<sup>TM</sup>. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 µg, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include <sup>90</sup>Y, <sup>123</sup>I, <sup>125</sup>I, <sup>131</sup>I, <sup>186</sup>Re, <sup>188</sup>Re, <sup>211</sup>At, and <sup>212</sup>Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, Pseudomonas exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulphydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulphydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis *et al. Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

The following Examples are offered by way of illustration and not by way of limitation.

### EXAMPLES

#### Example 1

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A<sup>+</sup> RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A<sup>+</sup> RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor

library contained  $1.64 \times 10^7$  independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained  $3.3 \times 10^6$  independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H<sub>2</sub>O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H<sub>2</sub>O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H<sub>2</sub>O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H<sub>2</sub>O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into

BamHI/XhoI site of chloramphenicol resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was

performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones; hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are

provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS:

93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively. cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

**Example 2****DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR  
POLYPEPTIDES**

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β-actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β-actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in

prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal

colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

### Example 3

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no

significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

#### Example 4

#### SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANTS: Xu, Jiangchun  
Dillin, Davin C.

(ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER  
AND METHODS FOR THEIR USE

(iii) NUMBER OF SEQUENCES: 224

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SEED and BERRY LLP  
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue  
(C) CITY: Seattle  
(D) STATE: WA  
(E) COUNTRY: USA  
(F) ZIP: 98104

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 23-FEB-1998  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.  
(B) REGISTRATION NUMBER: 31,392  
(C) REFERENCE/DOCKET NUMBER: 210121.427C3

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 622-4900  
(B) TELEFAX: (206) 682-6031

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTTTTTTTT TTTTCACAG TATAACAGCT CTTTATTCT GTGAGTTCTA CTAGGAAATC     | 60  |
| ATCAAATCTG AGGGTTGTCT GGAGGACTTC AATACACCTC CCCCCATAGT GAATCAGCTT  | 120 |
| CCAGGGGGTC CAGTCCCTCT CCTTACTTCA TCCCCATCCC ATGCCAAAGG AAGACCCCTCC | 180 |
| CTCCTTGGCT CACAGCCTTC TCTAGGCTTC CCAGTGCCTC CAGGACAGAG TGGGTTATGT  | 240 |
| TTTCAGCTCC ATCCTTGCTG TGAGTGTCTG GTGCCCTGTG CCTCCAGCTT CTGCTCAGTG  | 300 |
| CTTCATGGAC AGTGTCCAGC ACATGTCACT CTCCACTCTC TCAGTGTGGA TCCACTAGTT  | 360 |
| CTAGAGCGGC CGCCACCGCG GTGGAGCTCC AGCTTTGTT CCCTTAGTG AGGGTTAATT    | 420 |

|                                              |                                  |     |
|----------------------------------------------|----------------------------------|-----|
| GCGCGCTTGG CGTAATCATG GTCATAACTG             | TTTCCTGTGT GAAATTGTTA TCCGCTCACA | 480 |
| ATTCCACACA ACATACGAGC CGGAAGCATA AAGTGTAAAG  | CCTGGGGTGC CTAATGAGTG            | 540 |
| ANCTAACTCA CATTAAATTGC GTTGCCTCA CTGNCCGCTT  | TCCAGTCNGG AAAACTGTCG            | 600 |
| TGCCAGCTGC ATTAATGAAT CGGCCAACGC NCGGGGAAAAA | GCGGTTTGCG TTTTGGGGC             | 660 |
| TCTTCCGCTT CTCGCTCACT NANTCCTGCG CTCGGTCNTT  | CGGCTGCGGG GAACGGTATC            | 720 |
| ACTCCTCAAA GGNGGTATTA CGGTTATCCN NAAATCNGGG  | GATAACCNGG AAAAAANTTT            | 780 |
| AACAAAAGGG CANCAAAGGG CNGAAACGTA AAAA        |                                  | 814 |

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACAGAAATGT TGGATGGTGG AGCACCTTTC TATACGACTT ACAGGACAGC AGATGGGGAA | 60  |
| TTCATGGCTG TTGGAGCAAT AGAACCCCAG TTCTACGAGC TGCTGATCAA AGGACTTGGA | 120 |
| CTAAAGTCTG ATGAACTTCC CAATCAGATG AGCATGGATG ATTGGCCAGA AATGAAGAAG | 180 |
| AAGTTGCAAG ATGTATTTGC AAAGAAGACG AAGGCAGAGT GGTGTCAAAT CTTTGACGGC | 240 |
| ACAGATGCCCT GTGTGACTCC GGTTCTGACT TTTGAGGAGG TTGTTCATCA TGATCACAC | 300 |
| AAGGAACGGG GCTCGTTAT CACCAGTGAG GAGCAGGACG TGAGCCCCCG CCCTGCACCT  | 360 |
| CTGCTGTTAA ACACCCCAGC CATCCCTCTT TTCAAAAGGG ATCCACTAGT TCTAGAACG  | 420 |
| GCCGCCACCG CGGTGGAGCT CCAGCTTTG TTCCCTTAG TGAGGGTTAA TTGCGCGCTT   | 480 |
| GGCGTAATCA TGGTCATAGC TGTTCTCTGT GTGAAATTGT TATCCGCTCA CAATTCCCCC | 540 |
| AACATACGAG CGGAAACATA AAGTGTAAAG CCTGGGGTGC CTAATGANTG AGCTAACTCN | 600 |
| CATTAATTGC GTTGCCTCA CTGCCCGCTT TCCAGTCGGG AAAACTGTGC TGCCACTGCN  | 660 |
| TTANTGAATC NGCCACCCCC CGGGAAAAGG CGGTTGCNTT TTGGGCCTCT TCCGCTTCC  | 720 |
| TCGCTCATG ATCCTNGCNC CCGGTCTTCG GCTGGGNGA ACGGTTCACT CCTCAAAGGC   | 780 |
| GGTNTNCCGG TTATCCCCAA ACNGGGATA CCCNGA                            | 816 |

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| CTTTGAAAG AAGGGATGGC TGCGGGTGTAA AACAGCAGAG GTGCAGGGCG GGGGCTCACG  | 60  |
| TCCTGCTCCT CACTGGTGTAA ACACGAGCCC CGTTCTTGT TGTGATCATG ATGAAACAACC | 120 |
| TCCTCAAAAG TCAGAACCGG AGTCACACAG GCATCTGTGC CGTCAAAGAT TTGACACCAC  | 180 |
| TCTGCCCTCG TCTTCTTGC AAATACATCT GCAAACCTCT TCTTCATTTG TGCCCAATCA   | 240 |
| TCCATGCTCA TCTGATTGGG AAGTCATCA GACTTAGTC CANNTCCCTT GATCAGCAGC    | 300 |
| TCGTAGAACT GGGGTTCTAT TGCTCCAACA GCCATGAATT CCCCCTCTGC TGTCTGTAA   | 360 |
| GTCGTATAGA AAGGTGCTCC ACCATCCAAC ATGTTCTGTC CTCGAGGGGG GGGCCGGTAC  | 420 |
| CCAATTGCC CTATANTGAG TCGTATTACG CGCGCTCACT GGCCGTCGTT TTACAACGTC   | 480 |
| GTGACTGGGA AAACCCCTGGG CGTTACCAAC TTAATGCCT TGCAGCACAT CCCCCCTTCG  | 540 |
| CCAGCTGGGC GTAATANCAGA AAAGGCCGC ACCGATGCC CTTCCAACAG TTGCGCACCT   | 600 |
| GAATGGNAA ATGGGACCCC CCTGTTACCG CGCATTNAAC CCCCGCNGGG TTTNGTTGTT   | 660 |
| ACCCCCACNT NNACCGCTTA CACTTTGCCA GCGCCTTANC GCCCCGCTCCC TTTCNCCTTT | 720 |
| CTTCCCTTCC TTTCNCNCNN CTTTCCCCCG GGGTTTCCCC CNTCAAACCC CNA         | 773 |

## (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| CCTCCTGAGT CCTACTGACC TGTGCTTCT GGTGTGGAGT CCAGGGCTGC TAGGAAAAGG    | 60  |
| AATGGGCAGA CACAGGTGTA TGCCAATGTT TCTGAAATGG GTATAATTTC GTCCCTCTCCT  | 120 |
| TCGGAACACT GGCTGTCTCT GAAGACTTCT CGCTCAGTTT CAGTGAGGAC ACACACAAAG   | 180 |
| ACGTGGGTGA CCATGTTGT TGTGGGGTGC AGAGATGGGA GGGGTGGGCC CCACCCCTGGA   | 240 |
| AGACTGGACA GTGACACAAAG GTGGCACACTC TCTACAGATC ACTGAGGATA AGCTGGAGCC | 300 |
| ACAATGCATG AGGCACACAC ACAGCAAGGA TGACNCTGTA AACATAGCCC ACGCTGTCC    | 360 |
| GNGGGCCTAG GGAAGCCTAN ATNAGGGCTG GAGCANAAG AAGGGGAGGA TCCACTAGTT    | 420 |
| CTANAGCGGC CGCCACCGCG GTGGANCCTCC ANCTTTGTT CCCTTTAGTG AGGGTTAATT   | 480 |
| GCGCGCTTGG CNTAATCATG GTCATANCTN TTTCTGTGT GAAATTGTTA TCCGCTCACA    | 540 |
| ATTCCACACA ACATACGANC CGGAAACATA AANTGAAAC CTGGGGTGC TAATGANTGA     | 600 |
| CTAACTCACA TTAATTGCGT TCGCCTACT CGCCGCTTTC CAATCNGAA ACCTGTCTTG     | 660 |
| CCNCCTGCAT TNATGAATCN GCCAACCCCC GGGGAAAAGC GTTTGCGTT TGGGCCTCT     | 720 |
| TCCGCTTCCT CNCTCANTTA NTCCCTNCNC TCGGTCAATT CGGCTGCNGC AAACCGGTTTC  | 780 |
| ACCNCTCCA AAGGGGGTAT TCCGGTTTCC CCNAATCCGG GGANANCC                 | 828 |

## (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTTTTTTTTT TTTTTACTGA TAGATGGAAT TTATTAAGCT TTTCACATGT GATAGCACAT  | 60  |
| AGTTTTAATT GCATCCAAAG TACTAACAA AACTCTAGCA ATCAAGAATG GCAGCATGTT   | 120 |
| ATTTTATAAC AATCAACACC TGTGGCTTT AAAATTGTT TTTCATAGA TAATTTATAC     | 180 |
| TGAAGTAAAT CTAGCCATGC TTTTAAAAAA TGCTTTAGGT CACTCCAAGC TTGGCAGTTA  | 240 |
| ACATTTGGCA TAAACAATAA TAAAACAATC ACAATTAAAT AAATAACAAA TACAACATTG  | 300 |
| TAGGCCATAA TCATATACAG TATAAGAAA AGGTGGTAGT GTTGAGTAAG CAGTTATTAG   | 360 |
| AATAGAATAC CTTGGCCTCT ATGCAAATAT GTCTAGACAC TTTGATTACAC TCAGCCCTGA | 420 |
| CATTCACTTT TCAAAGTAGG AGACAGGTTTC TACAGTATCA TTTTACAGTT TCCAACACAT | 480 |
| TGAAAACAAG TAGAAAATGA TGAGTTGATT TTTATTAATG CATTACATCC TCAAGAGTTA  | 540 |
| TCACCAACCC CTCAGTTATA AAAAATTTC AAGTTATATT AGTCATATAA CTTGGTGTGC   | 600 |
| TTATTTAAA TTAGTGCTAA ATGGATTAAAG TGAAGACAAC AATGGTCCCC TAATGTGATT  | 660 |
| GATATTGGTC ATTTTACCA GCTTCTAAAT CTNAACTTTC AGGCTTTGTA ACTGGAACAT   | 720 |
| TGNATNACAG TGTTCCANAG TTNCAACCTA CTGGAACATT ACAGTGTGCT TGATTCAAA   | 780 |
| TGTTATTTG TTAAAAATTA AATTTAACCG TGGTGGAAAA ATAATTGAA ATNA          | 834 |

## (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTTTTTTTTT TTTTTTTTTT AAGACCCTCA TCAATAGATG GAGACATACA GAAATAGTCA  | 60  |
| AACCACATCT ACAAAATGCC AGTATCAGC CGCGGGCTTCG AAGCCAAAGT GATGTTGGA   | 120 |
| TGTAAAAGTGA AATATTAGTT GGCGGATGAA GCAGATAGTG AGGAAAGTTG AGCCAATAAT | 180 |
| GACGTGAAGT CCGTGGAAAGC CTGTGGCTAC AAAAATGTT GAGCCGTAGA TGCCGTCGGA  | 240 |
| AATGGTGAAG GGAGACTCGA AGTACTCTGA GGCTGTAGG AGGGTAAAAT AGAGACCCAG   | 300 |
| TAAAATTGTA ATAAGCAGTG CTTGAATTAT TTGGTTTCGG TTGTTTTCTA TTAGACTATG  | 360 |
| GTGAGCTCAG GTGATTGATA CTCCCTGATGC GAGTAATACG GATGTGTTTA GGAGTGGGAC | 420 |
| TTCTAGGGGA TTAGCGGGG TGATGCCGTG TGGGGCCAG TGCCCTCCTA GTTGGGGGT     | 480 |
| AGGGCTAGG CTGGAGTGGT AAAAGGCTCA GAAAAATCCT GCGAAGAAAA AAACCTCTGA   | 540 |
| GGTAATAAAT AGGATTATCC CGTATCGAAG GCCTTTTGG ACAGGTGGTG TGTGGTGGCC   | 600 |
| TTGGTATGTG CTTTCTCGTG TTACATCGCG CCATCATTGG TATATGGTTA GTGTGGTGGG  | 660 |
| TTANTANGGC CTANTATGAA GAACTTTGG ANTGAATTA AATCAATNGC TTGGCCGGAA    | 720 |
| GTCATTANGA NGGCTNAAA GGCCCTGTTA NGGGTCTGGG CTNGGTTTA CCCNACCCAT    | 780 |
| GGAATNCNCC CCCCGGACNA NTGNATCCCT ATTCTTAA                          | 818 |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTTTTTTTTT TTTTTTTTTT TGGCTCTAGA GGGGTAGAG GGGGTGCTAT AGGGTAAATA   | 60  |
| CGGGCCCTAT TTCAAAGATT TTTAGGGAA TAAATTCTAG GACGATGGGT ATGAAACTGT   | 120 |
| GGTTTGCTCC ACAGATTTCA GAGCATTGAC CGTAGTATAC CCCCCTGCGT GTAGCGGTGA  | 180 |
| AAGTGGTTG GTTGTAGACGT CCGGGAATTG CATCTGTTT TAAGCCTAAT GTGGGACAG    | 240 |
| CTCATGAGTG CAAGACGTCT TGTGATGAA TTATTATACN AATGGGGCT TCAATCGGA     | 300 |
| GTACTACTCG ATTGTCAACG TCAAGGAGT GCAGGTCGCC TGGTTCTAGG AATAATGGGG   | 360 |
| GAAGTATGTA GGAATTGAAG ATTAATCCCG CGTAGTCGGT GTTCTCCTAG GTCATGAA    | 420 |
| ATTGGTGGCC ATTGATTG ATGGTAAAGG GAGGGATCGT TGAACCTCGTC TGTATGTAA    | 480 |
| AGGATNCCTT NGGGATGGGA AGGCNATNAA GGACTANGGA TNAATGGCGG GCANGATATT  | 540 |
| TCAAACNGTC TCTANTTCCT GAAACGTCTG AAATGTTAAT AANAATTAAN TTTNGTTATT  | 600 |
| GAATNTTNNG GAAAAGGGCT TACAGGACTA GAAACCAAAT ANGAAAANTA ATNNNTAANGG | 660 |
| CNTTATCNIN AAAGGTNATA ACCNCTCTA TNATCCCACC CAATNGNATT CCCCACNCCNN  | 720 |
| ACNATTGGAT NCCCCANTTC CANAAANGGC CNCCCCCGG TGNANNCCNC CTTTTGTTCC   | 780 |
| CTTNANTGAN GTTATTTCNC CCCTNGCNTT ATCANCC                           | 817 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CATTTCCGGG TTTACTTTCT AAGGAAAGCC GAGCGGAAGC TGCTAACGTG GGAATCGGTG | 60  |
| CATAAGGAGA ACTTTCTGCT GGCACGCGCT AGGGACAAGC GGGAGAGCGA CTCCGAGCGT | 120 |

|                       |            |            |            |            |     |
|-----------------------|------------|------------|------------|------------|-----|
| CTGAAGCGCA CGTCCCAGAA | GGTGGACTTG | GCACTGAAAC | AGCTGGGACA | CATCCGCGAG | 180 |
| TACGAACAGC GCCTGAAAGT | GCTGGAGCGG | GAGGTCCAGC | AGTGTAGCCG | CGTCCTGGG  | 240 |
| TGGGTGGCCG ANGCTGANC  | CGCTCTGCC  | TGCTGCC    | ANGTGGGCCG | CCACCCCTG  | 300 |
| ACCTGCCTGG GTCCAAACAC | TGAGCCCTGC | TGGCGGACTT | CAAGGANAAC | CCCCACANG  | 360 |
| GGATTTGCT CCTANANTAA  | GGCTCATCTG | GGCCTCGGCC | CCCCCACCTG | GTTGGCCTTG | 420 |
| TCTTGANGT GAGCCCCATG  | TCCATCTGGG | CCACTGTCNG | GACCACCTT  | NGGGAGTGT  | 480 |
| CTCCTTACAA CCACANNATG | CCCGGCTCCT | CCCGAAACC  | ANTCCCANCC | TGNGAAGGAT | 540 |
| CAAGNCCTGN ATCCACTNNT | NCTANAACCG | GCCNNCCNG  | CNGTGGAAC  | CNCCTNTGT  | 600 |
| TCCTTTCTN TNAGGGTTAA  | TNNCGCCTTG | GCCTTNCCAN | NGTCCTNCNC | NTTTTCCNNT | 660 |
| GTTNAAAATTG TTANGCNCC | NCCNNTCCCN | CNNCNCCNAN | CCCGACCCNN | ANNTTNNANN | 720 |
| NCCTGGGGGT NCCNNCNGAT | TGACCCNNCC | NCCCTNTANT | TGCNTTNGGG | NNCNNTGCC  | 780 |
| CTTCCCTCT NGGGANNCG   |            |            |            |            | 799 |

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 801 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

|                        |            |            |            |            |     |
|------------------------|------------|------------|------------|------------|-----|
| ACGCCTTGAT CCTCCCAGGC  | TGGGACTGGT | TCTGGGAGGA | GCCGGGCATG | CTGTGGTTG  | 60  |
| TAANGATGAC ACTCCCAAAG  | GTGGTCTG   | AAGTGGCCCA | GATGGACATG | GGGCTCACCT | 120 |
| CAAGGACAAG GCCACCAGGT  | CGGGGGGCCG | AAGCCCACAT | GATCCTTA   | CTATGAGCAA | 180 |
| AATCCCCCTGT GGGGGCTTCT | CCTTGAAGTC | CGCCANCAGG | GCTCAGTCTT | TGGACCCANG | 240 |
| CAGGTCACTGG GTTGTNGNC  | CAACTGGGGG | CCNCAACGCA | AAANGGCNCA | GGGCCTCNGN | 300 |
| CACCCATCCCC ANGACGCCG  | TACACTNCTG | GACCTCCCNC | TCCACCACTT | TCATGCGCTG | 360 |
| TTCNTACCCG CGNATNTGTC  | CCANCTGTT  | CNGTGCNAC  | TCCANCTTCT | NGGACGTGCG | 420 |
| CTACATAACGC CGGGANTCNC | NCTCCGCTT  | TGTCCCTATC | CACGTNCCAN | CAACAAATT  | 480 |
| CNCNTANTG CACCNATTCC   | CACNTTNNC  | AGNTTTCCNC | NNCGNGCTTC | CTTNTAAAAG | 540 |
| GGTTGANCCC CGGAAAATNC  | CCCAAAGGG  | GGGGGCCNGG | TACCCAAC   | CCCCCTNATA | 600 |
| GCTGAANTCC CCATNACNN   | GNCTCNATGG | ANCCNTCCNT | TTAANNACN  | TTCTNAACTT | 660 |
| GGGAANANCC CTCGNCCNT   | CCCCNTTAA  | TCCCNCCNTG | CNANGNNCNT | CCCCNNNTCC | 720 |
| NCCCNNTNG GCNTNTNANN   | CNAAAAAGGC | CCNNNANCAA | TCTCCTNNCN | CCTCANTTCG | 780 |
| CCANCCCTCG AAATCGGCCN  | C          |            |            |            | 801 |

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 789 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

|                       |            |            |            |            |     |
|-----------------------|------------|------------|------------|------------|-----|
| CAGTCTATNT GGCCAGTGTG | GCAGCTTCCC | CTGTGGCTGC | CGGTGCCACA | TGCCTGTCCC | 60  |
| ACAGTGTGGC CGTGGTGACA | GCTTCAGCCG | CCCTCACCGG | GGTCACCTTC | TCAGCCCTGC | 120 |
| AGATCCTGCC CTACACACTG | GCCTCCCTCT | ACCACCGGG  | GAAGCAGGTG | TTCCTGCCA  | 180 |
| AATACCGAGG GGACACTGG  | GGTGTAGCA  | GTGAGGACAG | CCTGATGACC | AGCTTCCTGC | 240 |
| CAGGCCCTAA GCCTGGAGCT | CCCTCCCTA  | ATGGACACGT | GGGTGCTGGA | GGCAGTGGCC | 300 |
| TGCTCCACC TCCACCCGCG  | CTCTGCGGGG | CCTCTGCC   | TGATGTCTCC | GTACGTGTGG | 360 |
| TGGTGGGTGA GCCCACCGAN | GCCAGGGTGG | TTCCGGGCCG | GGGCATCTGC | CTGGACCTCG | 420 |
| CCATCCTGGA TAGTGCTTCC | TGCTGTCCA  | NGTGGCCCCA | TCCCTGTTA  | TGGGCTCCAT | 480 |
| TGTCCAGCTC AGCCAGTCTG | TCACTGCCTA | TATGGTGTCT | GCCGCAGGCC | TGGGTCTGGT | 540 |

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CCCATTTACT TTGCTACACA GGTANTATT GACAAGAACG ANTTGGCCAA ATACTCAGCG  | 600 |
| TTAAAAAATT CCAGCAACAT TGGGGGTGGA AGGCCTGCCT CACTGGGTCC AACTCCCCGC | 660 |
| TCCTGTTAAC CCCATGGGC TGCCGGCTTG GCCGCCATT TCTGTTGCTG CCAAANTNAT   | 720 |
| GTGGCTCTCT GCTGCCACCT GTTGCTGGCT GAAGTGCNTA CNGNCANCT NGGGGGTNG   | 780 |
| GGNGTTCCCC                                                        | 789 |

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| CCCACCCCTAC CCAAATATTAA GACACCAACA CAGAAAAGCT AGCAATGGAT TCCCCTCTAC | 60  |
| TTTGTAAAT AAATAAGTTA AATATTAAA TGCCTGTGTC TCTGTGATGG CAACAGAAGG     | 120 |
| ACCAACAGGC CACATCCTGA TAAAAGTAA GAGGGGGGTG GATCAGCAA AAGACAGTGC     | 180 |
| TGTGGGCTGA GGGGACCTGG TTCTTGTGTT TTGCCCTCTCA GGACTCTTCC CCTACAAATA  | 240 |
| ACTTTCATAT GTTCAAATCC CATGGAGGAG TGTTCATCC TAGAAACTCC CATGCAAGAG    | 300 |
| CTACATTAAA CGAACGTGCA GGTAAAGGGG CTTANAGATG GGAAACCAGG TGACTGAGTT   | 360 |
| TATTCAGCTC CCAAAACCCC TTCTCTAGGT GTGTCTCAAC TAGGAGGCTA GCTGTTAAC    | 420 |
| CTGAGCCTGG GTAATCCACC TGCAGAGTCC CGCATTCCA GTGCATGGAA CCCITCTGGC    | 480 |
| CTCCTGTAT AAGTCCAGAC TGAAACCCCC TTGGAAGGNC TCCAGTCAGG CAGCCCTANA    | 540 |
| AACTGGGAA AAAAGAAAAG GACGCCCAN CCCCCAGCTG TGCANCTAG CACCTCAACA      | 600 |
| GCACAGGGTG GCAGAAAAAA ACCACTTTA CTTTGGCACA AACAAAAACT NGGGGGGGCA    | 660 |
| ACCCGGCAC CCCNANGGG GTTAACAGGA ANCNGGNAA CNTGGAACCC AATTNAGGCA      | 720 |
| GGCCCNCCAC CCCNAATNTT GCTGGGAAAT TTTCTCTCCC CTAAATTNTT TC           | 772 |

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GCCCCAATTC CAGCTGCCAC ACCACCCACG GTGACTGCAT TAGTCGGAT GTCATACAAA  | 60  |
| AGCTGATTGA AGCAACCCCTC TACTTTTG TGCTGAGCCT TTGCTTGGT GCAGGTTTCA   | 120 |
| TTGGCTGTGT TGGTGAAGTT GTCATTGCAA CAGAATGGGG GAAAGGCAGT GTTCTCTTG  | 180 |
| AAGTANGGTG AGTCTCTAAA ATCCGTATAG TTGGTGAAGC CACAGCACTT GAGCCCTTTC | 240 |
| ATGGTGGTGT TCCACACTTG AGTGAAGTCT TCCTGGGAAC CATAATCTTT CTTGATGGCA | 300 |
| GGCACTACCA GCAACGTGAG GGAAGTGTG AGCCATTGTG GTGTACACCA AGGCGACCCAC | 360 |
| AGCAGCTGCN ACCTCAGCAA TGAAGATGAN GAGGAGATG AAGAAGAACG TCNCGAGGGC  | 420 |
| ACACTTGCTC TCAGTCTTAN CACCATANCA GCCCTGAAA ACCAANANCA AAGACACNA   | 480 |
| CNCCGGCTGC GATGAAGAAA TNACCCNCG TTGACAAACT TGCATGGCAC TGGGANCCAC  | 540 |
| AGTGGCCCNAAAATCTCA AAAAGGATGC CCCATCNATT GACCCCCCAA ATGCCCACTG    | 600 |
| CCAACAGGGG CTGCCCCACN CNCNNACGA TGANCCNATT GNACAAGATC TNCNTGGTCT  | 660 |
| TNATNAACNT GAACCTGCN TNGTGGCTCC TGTTCAGGNC CNNGGCCTGA CTTCTNAANN  | 720 |
| AANGAACTCN GAAGNCCCCA CNGGANANN C                                 | 751 |

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| GAGCCAGGCG | TCCCTCTGCC | TGCCCACCTCA | GTGGCAACAC | CCGGGAGCTG | TTTTGTCCTT  | 60  |
| TGTGGANCCT | CAGCAGTNCC | CTCTTCAGA   | ACTCANTGCC | AAGANCCCTG | AAACAGGAGCC | 120 |
| ACCATGCAGT | GCTTCAGCTT | CATTAAGACC  | ATGATGATCC | TCTTCAATT  | GCTCATCTT   | 180 |
| CTGTGTGGTG | CAGCCCTGTT | GGCAGTGGGC  | ATCTGGGTGT | CAATCGATGG | GGCATCCTT   | 240 |
| CTGAAGATCT | TCGGGCCACT | GTCGTCCAGT  | GCCATGCAGT | TTGTCAACGT | GGGCTACTTC  | 300 |
| CTCATCGCAG | CCGGCGTTGT | GGTCTTAGCT  | CTAGGTTTCC | TGGGCTGCTA | TGGTGCTAAG  | 360 |
| ACTGAGAGCA | AGTGTGCCCT | CGTGACGTT   | TTCTCATCC  | TCCTCCTCAT | CTTCATTGCT  | 420 |
| GAGGTGCAA  | TGCTGTGGTC | GCCTTGGTGT  | ACACACAAAT | GGCTGAGCAC | TTCCCTGACGT | 480 |
| TGCTGGTAAT | GCCTGCCATC | AANAAAAGAT  | TATGGTTCC  | CAGGAANACT | TCACTCAAGT  | 540 |
| GTTGGAACAC | CACCATGAAA | GGGCTCAAGT  | GCTGTGGCTT | CNNCCAACTA | TACGGATT    | 600 |
| GAAGANTCAC | CTACTTCAAA | AAAAANAGTG  | CCTTCCCCC  | ATTCTGTTG  | CAATTGACAA  | 660 |
| ACGTCCCCAA | CACAGCCAAT | TGAAAACCTG  | CACCCAACCC | AAANGGGTCC | CCAACCANAA  | 720 |
| ATTNAAGGG  |            |             |            |            |             | 729 |

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 816 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| TGCTCTTCCT  | CAAAGTTGTT  | CTTGTGCCA  | TAACAACAC  | CATAGGTAAA | GGGGGCGCAG  | 60  |
| TGTTCGCTGA  | AGGGGTGTA   | GTACCAGCG  | GGGATGCTCT | CCTTGCAGAG | TCCCTGTGTCT | 120 |
| GGCAGGTCCA  | CGCAGTCCCC  | TTTGTCACTG | GGGAAATGGA | TGCGCTGGAG | CTCGTCAAAG  | 180 |
| CCACTCGTGT  | ATTTTTCACA  | GGCAGCCTCG | TCCGACGCGT | CGGGGCAGTT | GGGGGTGTCT  | 240 |
| TCACACTCCA  | GGAAACTGTC  | NATGCAGCAG | CCATTGCTGC | AGCGGAACTG | GGTGGGCTGA  | 300 |
| CANGTGCAG   | AGCACACTGG  | ATGGCGCCTT | TCCATGNAN  | GGGCCCTGNG | GGAAAGTCCC  | 360 |
| TGANCCCCAN  | ANCTGCCTCT  | CAAANGCCC  | ACCTTGCACA | CCCCGACAGG | CTAGAATGGA  | 420 |
| ATCTTCTTCC  | CGAAAGGTAG  | TTNTTCTTGT | TGCCCAANCC | ANCCCCNTAA | ACAAACTCTT  | 480 |
| GCANATCTGC  | TCCGNNGGGG  | TCNTANTACC | ANCGTGGAA  | AAGAACCCCA | GGCNGCGAAC  | 540 |
| CAANCTTGTT  | TGGATNCGAA  | GCNATAATCT | NCTNTTCTGC | TTGGTGGACA | GCACCANTNA  | 600 |
| CTGTNNNANCT | TTAGNCCNTG  | GTCCCTCN   | GTTGNNCTTG | AACCTAATCN | CCNNNTCAACT | 660 |
| GGGACAAGGT  | AANTNGCCNT  | CCTTNAATT  | CCCNANCNTN | CCCCCTGGTT | TGGGGTTTTN  | 720 |
| CNCNCTCTA   | CCCCAGAAAAN | NCCGTGTCC  | CCCCCAACTA | GGGGCCNAAA | CCNNTNTTC   | 780 |
| CACAACCCTN  | CCCCACCCAC  | GGGTCNGNT  | GGTTNG     |            |             | 816 |

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 783 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

|            |             |            |            |             |             |     |
|------------|-------------|------------|------------|-------------|-------------|-----|
| CCAAGGCCTG | GGCAGGCATA  | NACTTGAAGG | TACAACCCCA | GGAACCCCTG  | GTGCTGAAGG  | 60  |
| ATGTGGAAAA | CACAGATTGG  | CGCCTACTGC | GGGGTGACAC | GGATGTCAGG  | GTAGAGAGGA  | 120 |
| AAGACCCAAA | CCAGGTGGAA  | CTGTGGGAC  | TCAAGGAANG | CACCTACCTG  | TTCCAGCTGA  | 180 |
| CAGTGACTAG | CTCAGACCAC  | CCAGAGGACA | CGGCAACGT  | CACAGTCACT  | GTGCTGTCCA  | 240 |
| CCAAGCAGAC | AGAAGACTAC  | TGCCTCGCAT | CCAACAANGT | GGTCGCTGC   | CGGGGCTCTT  | 300 |
| TCCCACGCTG | GTACTATGAC  | CCCACGGAGC | AGATCTGCAA | GAGTTTCGTT  | TATGGAGGCT  | 360 |
| GCTTGGGCAA | CAAGAACAAAC | TACCTTCGGG | AAGAAGAGTG | CATTCTANCC  | TGTCNGGTG   | 420 |
| TGCAAGGTGG | GCCTTGANA   | NGCANCTCTG | GGGTCANGC  | GACTTTCCCC  | CAGGGCCCC   | 480 |
| CCATGGAAAG | GCGCCATCCA  | NTGTTCTCTG | GCACCTGTCA | GCCCACCCAG  | TTCCGCTGCA  | 540 |
| NCAATGGCTG | CTGCATCNAC  | ANTTCTCTNG | AATTGTGACA | ACACCCCCCA  | NTGCCCCAA   | 600 |
| CCCTCCCAAC | AAAGCTTCCC  | TGTTAAAAAA | TACNCCANTT | GGCTTTTNAC  | AAACNCCCGG  | 660 |
| CNCTCCNTT  | TTCCCCNNNT  | AACAAAGGGC | NCTNGCNTT  | GAAC TGCCCN | AAACCCNGGAA | 720 |
| TCTNCCNNNG | AAAANTNCC   | CCCCCTGGTT | CCTTNAANCC | CCTCCNCNA   | ANCTNCCCCC  | 780 |
| CCC        |             |            |            |             |             | 783 |

## (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| GCCCCAATT  | CAGCTGCCAC  | ACCACCCACG | GTGACTGCAT | TAGTTCGGAT | GTCATACAAA  | 60  |
| AGCTGATTGA | AGCAACCCCTC | TACTTTTGG  | TCGTGAGCCT | TTGCTTGGT  | GCAGGTTCA   | 120 |
| TTGGCTGTGT | TGGTGACGTT  | GTCATTGCAA | CAGAATGGGG | GAAAGGCACT | GTTCTCTTG   | 180 |
| AAGTAGGGTG | AGTCCTCAAA  | ATCCGTATAG | TTGGTGAAGC | CACAGCACTT | GAGCCCTTC   | 240 |
| ATGGTGGTGT | TCCACACTTG  | AGTGAAGTCT | TCCTGGAAC  | CATAATCTTT | CTTGATGGCA  | 300 |
| GGCACTACCA | GCAACGTCAG  | GAAGTGCCTA | GCCATTGTGG | TGTACACCAA | GGCGACCACA  | 360 |
| GCAGCTGCAA | CCTCAGCAAT  | GAAGATGAGG | AGGAGGATGA | AGAAGAACGT | CNCGAGGGCA  | 420 |
| CACTTGCTCT | CCGTCTTACG  | ACCATAGCAG | CCCANGAAAC | CAAGAGCAAA | GACCACAAACG | 480 |
| CCNGCTGCGA | ATGAAAGAAA  | NTACCCACGT | TGACAAACTG | CATGGCCACT | GGACGACAGT  | 540 |
| TGGCCCGAAN | ATCTTCAGAA  | AAGGGATGCC | CCATCGATTG | AACACCCANA | TGCCCACGTGC | 600 |
| CNACAGGGCT | GCNCNCNCN   | GAAAGAATGA | GCCATTGAAG | AAGGATCNTC | NTGGTCTTAA  | 660 |
| TGAAGTAAA  | CNTGCATGG   | TGGCCCTGT  | TCAGGGCTCT | TGGCAGTGAA | TTCTGANAAA  | 720 |
| AAGGAACNGC | NTNAGCCCC   | CCAAANGANA | AAACACCCCA | GGGTGTTGCC | CTGAATTGGC  | 780 |
| GGCCAAGGAN | CCCTGCCCN   | G          |            |            |             | 801 |

## (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GTGAGAGCCA | GGCGTCCCTC | TGCCTGCCA  | CTCAGTGGCA | ACACCCGGGA | GCTGTTTGT  | 60  |
| CCTTTGTGGA | GCCTCAGCAG | TTCCCTCTT  | CAGAACTCAC | TGCCAAGAGC | CCTGAACAGG | 120 |
| AGCCACCATG | CAGTGCTTCA | GCTTCATTAA | GACCATGATG | ATCCTCTTCA | ATTTGCTCAT | 180 |
| CTTTCTGTGT | GGTGCAGCCC | TGTTGGCAGT | GGGCATCTGG | GTGTCAATCG | ATGGGGCATC | 240 |
| CTTTCTGAAG | ATCTTCGGGC | CACTGTCGTC | CAGTGCATG  | CAGTTGTCA  | ACGTGGCTA  | 300 |
| CTTCCTCATC | GCAGCCGGCG | TTGTGGTCTT | TGCTCTTGGT | TTCCTGGGCT | GCTATGGTGC | 360 |

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| TAAGACGGAG AGCAAGTGTG CCCTCGTGAC GTTCTTCTTC ATCCTCCTCC TCATCTTCAT   | 420 |
| TGCTGAAGTT GCAGCTGCTG TGGTCGCCTT GGTGTACACC ACAATGGCTG AACCAATTCCCT | 480 |
| GACGTTGCTG GTANTGCCTG CCATCAANAA AGATTATGGG TTCCCAAGGAA AAATTCACTC  | 540 |
| AANTNTGGAA CACCNCCATG AAAAGGGCTC CAATTCTGN TGCCCTTCCCC AACTATAACG   | 600 |
| GAATTTGAA AGANTCNCCC TACTTCCAAA AAAAANANT TGCCCTTNCC CCCNTTCTGT     | 660 |
| TGCAATGAAA ACNTCCAAN ACNGCCAATN AAAACCTGCC CNNNCNNAAA GGNTCNCAA     | 720 |
| CAAAAAAANT NNAAGGGTTN                                               | 740 |

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| CCGCTGGTTG CGCTGGTCCA GNNGNAGCCAC GAAGCACGTC AGCATACACA GCCTCAATCA | 60  |
| CAAGGTCTTC CAGCTGCCG ACATTACGCA GGGCAAGAGC CTCCAGCAAC ACTGCATATG   | 120 |
| GGATACACTT TACTTTAGCA GCCAGGGTGA CAACTGAGAG GTGTCGAAGC TTATTCTTCT  | 180 |
| GAGCCTCTGT TAGTGGAGGA AGATTCGGGG CTTCAGCTAA GTAGTCAGCG TATGTCCCAT  | 240 |
| AAGCAAACAC TGTGAGGCAGC CGGAAGGTAG AGGCAGAAC ACTCTCAGCC AGCTCTCTAA  | 300 |
| CATTGGGCAT GTCCAGCAGT TCTCAAACA CGTAGACACC AGNGGCCTCC AGCACCTGAT   | 360 |
| GGATGAGTGT GGCCAGCGCT GCCCCCTTGG CCGACTTGGC TAGGAGCAGA AATTGCTCT   | 420 |
| GGTTCTGCCG TGTCACTTC ACTTCCGCAC TCATCACTGC ACTGAGTGTG GGGGACTTGG   | 480 |
| GCTCAGGATG TCCAGAGACG TGGTTCCGCC CCCTCNCTTA ATGACACCGN CCANNCAACC  | 540 |
| GTCGGCTCCC GCGCANTGNG TTCGTCGTNC CTGGTCAGG GTCTGCTGGC CNCTACTTGC   | 600 |
| AANCTTCGTC NGGGCCATGG AATTCAACNC ACCGGAACTN GTANGATCCA CTNNNTCTAT  | 660 |
| AACCGGNCGC CACCGCNNTT GGAACCTCCAC TCTTNTTNCC TTTACTTGAG GGTTAAGGTC | 720 |
| ACCCCTNNCG TTACCTTGGT CCAAACCTNT CCNTGTGTCG ANATNGTNAA TCNGGNCCNA  | 780 |
| TNCCANCCNC ATANGAAGCC NG                                           | 802 |

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| CNAAGCTTCC AGGTNACGGG CGCNAANCC TGACCCNAGG TANCANAANG CAGNCNGCG    | 60  |
| GAGCCCACCG TCACGNGNG GNGTCTTAT NGGAGGGGGC GGAGCCACAT CNCTGGACNT    | 120 |
| CNTGACCCCA ACTCCCNCC NCNCANTGCA GTGATGAGTG CAGAACTGAA GGTNACGTGG   | 180 |
| CAGGAACCAA GANCAAANNC TGCTCCNNTC CAAGTCGGCN NAGGGGGCGG GGCTGGCCAC  | 240 |
| GCNCATCCNT CNAGTGCTGN AAAGCCCCNN CCTGTCTACT TGTTGGAGA ACNGCENNNA   | 300 |
| CATGCCCAAGN GTTANATAAC NGGCNGAGAG TNANTTTGCC TCTCCCTTCC GGCTGCGCAN | 360 |
| CGNGTNTGCT TAGNGGACAT AACCTGACTA CTTAACTGAA CCCNNGAATC TNCCNCCCT   | 420 |
| CCACTAAGCT CAGAACAAAA AACTTCGACA CCACTCANTT GTCACCTGNC TGCTCAAGTA  | 480 |
| AAGTGTACCC CATNCCCAAT GTNTGCTNGA NGCTCTGNCC TGCNTTANGT TCGGTCTGG   | 540 |
| GAAGACCTAT CAATTNAAGC TATGTTCTG ACTGCCCTTT GCTCCCTGNA ACAANCNACC   | 600 |
| CNNCNNTCCA AGGGGGGGNC GGCCCCAAT CCCCCCAACC NTNAATTNAN TTTANCCCN    | 660 |
| CCCCNGGCC CGGCCTTTA CNANCNTCN NNACNGGNA AAACCNNGC TTNCCCAAC        | 720 |
| NNAATCCNCC T                                                       | 731 |

## (2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| TTTTTTTTTT TTTTTTTTTT TAAAAACCCC CTCCATTNAA TGNAAACTTC CGAAATTGTC   | 60  |
| CAACCCCCCTC NTCCAAATNN CCNTTTCGG GNNGGGGTTC CAAACCCAAN TTANNTTTGG   | 120 |
| ANNTTAAATT AAATNTTNTT TGGNGGNNA ANCCNAATGT NANGAAAGTT NAACCCANTA    | 180 |
| TNANCTTNAA TNCCCTGGAAA CCNGTNGNTT CCAAAAATNT TTAACCCCTTA ANTCCCTCCG | 240 |
| AAATNGTTNA NGGAAAACCC AANTTCTCT AAGGGTGTGTT GAAGGNTNAA TNAAAANCCC   | 300 |
| NNCCAAATTGT TTTTNGCCAC GCCTGAATTA ATTGGNTTCC GNTGTTTCC NTTAAAANAA   | 360 |
| GGNNANCCCC GGTTANTNAA TCCCCCNCCN CCAAATTATA CCGANTTTTT TTNGAATTGG   | 420 |
| GANCCCNCGG GAATTAACGG GGNNNNNTCCC TNTTGGGGGG CNGGNNNNCCC CCCCNTCGGG | 480 |
| GGTTNGGGNC AGGNCCNAAT TGTTTAAGGG TCCGAAAAT CCCCTCNAGA AAAAAANCTC    | 540 |
| CCAGGNTGAG NNTNGGGTTT NCCCCCCCCC CANGGCCCT CTCGNANAGT TGGGGTTTGG    | 600 |
| GGGGCCTGGG ATTTTNTTTC CCCTNTTNC TCCCCCCCCC CCNGGGANAG AGGTTNGNGT    | 660 |
| TTTGNTCNC GGCCCCNCCN AAGANTTN CCGANTTNAN TAAATCCNT GCCTNGGCAG       | 720 |
| AGTCCTTGN AGGGNTAAAN GGCCCCCTNN CGGG                                | 754 |

## (2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ATCANCCCAT GACCCCNAAAC NNNGGACCNC TCANCCGGNC NNNCNACCNC CGGCCNATCA  | 60  |
| NNGTNAGNNC ACTCNNTTN NATCACNCCC CNCCNACTAC GCCCNANC CNACGCNCTA      | 120 |
| NNCANATNCC ACTGANNGCG CGANGTNGAN NGAGAAAANCT NATACCANAG NCACCCANACN | 180 |
| CCAGCTGTCC NANAANGCT NNNATACNGG NNNATCCAAT NTGNANCCTC CNAAGTATTN    | 240 |
| NNCNCCNAT GATTTTCCCTN ANCCGATTAC CCNTNCCCCC TANCCCCCTCC CCCCCAACNA  | 300 |
| CGAAGGCNCT GGNCCNAAGG NNCGCNCCN CCGCTAGNTC CCCNNCAAGT CNCNCNCTA     | 360 |
| AACTCANCCN NATTACNCGC TTCNTGAGTA TCACTCCCCG AATCTCACCC TACTCAACTC   | 420 |
| AAAAANATCN GATAACAAAT AATNCAAGCC TGNTTATNAC ACTNTGACTG GGTCTCTATT   | 480 |
| TTAGNGGTCC NTNAANCNTC CTAATACTTC CAGTCTNCCT TCNCCAATT CCNAANGGCT    | 540 |
| CTTTCNGACA GCATNTTTTG GTTCCCNNTT GGGTTCTTAN NGAATTGCC CTCNTNGAAC    | 600 |
| GGGCTCNTCT TTTCCTTCGG TTANCCTGGN TTCNNCCGGC CAGTTATTAT TTCCCNNTTT   | 660 |
| AAATTCTNCC CNTTTANTTT TGGCCTTCNA AACCCCCGGC CTTGAAAACG GCCCCCTGGT   | 720 |
| AAAAGGTTGT TTTGANAAAAA TTTTTGTTTT GTTCC                             | 755 |

## (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTTTTTTTTT TTTTTTANGTG TNGTCGTGCA CGTAGAGGCT TACTACAANT GTGAANACGT | 60  |
| ACGCTNGGAN TAANGCGACC CGANTTCTAG GANNCCCTT AAAATCANAC TGTGAAGATN   | 120 |
| ATCTGNMNA CGGAANGGTC ACCGGNNNGAT NNTGCTAGGG TGNCCNCTCC CANNNCNTTN  | 180 |
| CATAACTCNG NGGCCCTGCC CACCACCTTC GGCGGCCNG NGNCCGGGCC CGGGTCATTN   | 240 |
| GNNTTAACCN CACTNNGCNA NCAGGTTCCN NCCCCNNCNG ACCCNNGCGA TCCGGGGTNC  | 300 |
| TCTGTCTTCC CCTGNAGNCN ANAAANTGGG CCNCGGNCCC CTTTACCCCT NNACAAAGCCA | 360 |
| CNGCCNTCTA NCCNCNGCCC CCCCTCCANT NNGGGGGACT GCCNANNGCT CCGTTNCTNG  | 420 |
| NNACCCNNN GGGTNCCTCG GTTGTGANT CNACCGNANG CCANGGATTG CNAAGGAAGG    | 480 |
| TGCGTTNTTG GCCCCCTACCC TTGCTNCGG NNCACCCCTTC CCGACNANGA NCCGCTCCCG | 540 |
| CNCNCGNNG CCTCNCCCTCG CAACACCCGC NCTNTCNGT NCAGGNNNCCC CCCCACCCGC  | 600 |
| NCCCTNCNC NGNCGNANCN CTCCNCCNCC GTCTCANNCA CCACCCCGCC CCGCCAGGCC   | 660 |
| NTCANCCACN GGNNGACNN NAGCNCNTC GCNCCGCGN GCGNCNCCT CGCCNCNGAA      | 720 |
| CTNCNTCNGG CCANTNNCGC TCAANCCNNA CNAAACGCCG CTGCGCGGCC CGNAGCGNCC  | 780 |
| NCCTCCNGA GTCCCTCCGN CTTCCNACCC ANGNNNTCCN CGAGGACACN NNACCCCGCC   | 840 |
| NNCANGCGG                                                          | 849 |

## (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 872 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GCGCAAACTA TACTTCGCTC GNACTCGTC GCCTCGCTNC TCTTTTCCTC CGCAACCATG  | 60  |
| TCTGACNANC CCGATTNGGC NGATATCNAN AAGNTCGANC AGTCCAAACT GANTAACACA | 120 |
| CACACNCNAN AGANAAATCC NCTGCCTTCC ANAGTANACN ATTGAACNN AGAACCAANGC | 180 |
| NGGCGAATCG TAATNAGGC TGCGCCGCCA ATNTGTCNCC GTTTATTNTN CCAGCNTCNC  | 240 |
| CTNCCNACCC TACNTCTTCN NAGCTGTCNN ACCCCTNGTN CGNACCCCCC NAGGTCGGGA | 300 |
| TCGGGTTNN NNTGACCGNG CNNCCCTCC CCCCNCCAT NACGANCCNC CCGCACCCACC   | 360 |
| NANNGCNCGC NCCCCGNCTCCTTGCCNCC CTGCTCTNTN CCCCTGTNGC CTGGCNCNGN   | 420 |
| ACCGCATTGA CCCTCGCCNN CTNCNNGAAA NCGNANACGT CCGGGTTGNN ANNANCCTG  | 480 |
| TGGGNNNGCG TCTGCNCCGC GTTCTTCCN NCNNCTCCA CCATCTTCNT TACNGGTCT    | 540 |
| CCNCGCTTC TCNNNCACNC CCTGGGACGC TNTCCTNTGC CCCCCCTTNAC TCCCCCCCTT | 600 |
| CGNCGTGNCC CGNCCCCACC NTCATTTNCA NACGNTCTTC ACAANNNCCT CGNTNNCTCC | 660 |
| CNANCNGNCN GTCANCCNAG GGAAGGGNGG GGNNCNNNTG NTGACGTTG NGNGANGTC   | 720 |
| CGAANANTCC TCNCNTCANCNCTACCCCT CGGGCGNNCT CTCNGTTNCC AACTTANCAA   | 780 |
| NTCTCCCCCG NGNGCNCNTC TCAGCCTCNC CCNCCCCNCT CTCTGCANTG TNCTCTGCTC | 840 |
| TNACCNNTAC GANTNTTCGN CNCCCTCTTT CC                               | 872 |

## (2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 815 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GCATGCAAGC TTGAGTATTTC TATAGNGTCA CCTAAATANC TTGGCNTAAT CATGGTCNTA | 60  |
| NCTGNCTTCC TGTGTCAAAT GTATACNAAN TANATATGAA TCTNATNTGA CAAGANNGTA  | 120 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TCNTNCATTA | GTAACAANTG | TNNTGTCCAT | CCTGTCNGAN | CANATTCCC  | TNNATTNCGN | 180 |
| CGCATTNCN  | GCNCANTATN | TAATNGGGAA | NTCNNTNNN  | NCACNNCAT  | CTATCNTCC  | 240 |
| GCNCCTGAC  | TGGNAGAGAT | GGATNANTTC | TNNNTGACC  | NACATGTTCA | TCTTGGATTN | 300 |
| AANANCCCC  | CGCNGNCCAC | CGGTTNGNG  | CNAGCCNNTC | CCAAGACCTC | CTGTGGAGGT | 360 |
| AACCTGCGTC | AGANNCATCA | AACNTGGAA  | ACCCGCNNCC | ANGTNNAAGT | NGNNNCANAN | 420 |
| GATCCCCTC  | AGGNTTNACC | ATCCCTTCNC | AGCGCCCCCT | TTNGTGCCTT | ANAGNGNAGC | 480 |
| GTGTCNANC  | CNCTCAACAT | GANACGCC   | AGNCCANCCG | CAATNGGCA  | CAATGTCNC  | 540 |
| GAACCCCCA  | GGGGGANTNA | TNCAAANCCC | CAGGATTGTC | CNCNCANGAA | ATCCCNCANC | 600 |
| CCCNCCCTAC | CCNNCTTGG  | GACNGTGACC | AANTCCCGGA | GTNCCAGTCC | GGCCNGNCTC | 660 |
| CCCCACCGGT | NNCCNTGGGG | GGGTGAANCT | CNGNNTCANC | CNGNCAGGN  | NTCGNAAGGA | 720 |
| ACCGNCNCTN | GGNCGAANNG | ANCNNTCNGA | AGNGCCNCNT | CGTATAACCC | CCCCTCNCCA | 780 |
| NCCNACNGNT | AGNTCCCCCC | CNGGGTNCGG | AANGG      |            |            | 815 |

## (2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| CCGAGATGTC | TCGCTCCGTG | GCCTTAGCTG | TGCTCGCGCT | ACTCTCTCTT  | TCTGGCCTGG | 60  |
| AGGCTATCCA | CGTACTCCA  | AAGATTCAAG | TTTACTCAGC | TCATCCAGCA  | GAGAATGGAA | 120 |
| AGTCAAATTT | CCTGAATTGC | TATGTGTC   | GGTTTCATCC | ATCCGACATT  | GAANTTGACT | 180 |
| TACTGAAGAA | TGGANAGAGA | ATTGAAAAAG | TGGAGCATTC | AGACTTGTCT  | TTCAGCAAGG | 240 |
| ACTGGTCTTT | CTATCTCNTG | TACTACACTG | AATTCCACCC | CACTGAAAAA  | GATGAGTATG | 300 |
| CCTGCCGTGT | GAACCATGTG | ACTTTGTCA  | AGCCCAAGAT | AGTTAAGTGG  | GATCGAGACA | 360 |
| TGTAAGCAGN | CNNCATGGAA | GTTTGAAGAT | GCCGCAATTG | GATTGGATGA  | ATTCCAAATT | 420 |
| CTGCTTGCTT | GCNTTTAAT  | ANTGATATGC | NTATACACCC | TACCTTTAT   | GNCCCCAAAT | 480 |
| TGTAGGGGTT | ACATNANTGT | TCNCNTNGGA | CATGATCTTC | CTTTATAAANT | CCNCCNTTCG | 540 |
| AATTGCCCGT | CNCCCGTNT  | NGAATGTTTC | CNNAACCACG | GTGGCTCCC   | CCAGGTCNCC | 600 |
| TCTTACGGAA | GGGCTGGGC  | CNCTTNCAA  | GGTTGGGGGA | ACCNAAAATT  | TCNCTNTGC  | 660 |
| CCNCCCNCA  | CNNTCTTGNG | NNNCANTTT  | GGAACCCCTC | CNATTCCCT   | TGGCCTCNNA | 720 |
| NCCTNNCTA  | ANAAAACTTN | AAANCNTNGC | NAAANNTTTN | ACTTCCCCCC  | TTACC      | 775 |

## (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ANATTANTAC | AGTGTAATCT | TTTCCCAGAG | GTGTGTANAG | GGAACGGGGC | CTAGAGGCAT | 60  |
| CCCANAGATA | NCTTATANCA | ACAGTGCTTT | GACCAAGAGC | TGCTGGGCAC | ATTCCTGCA  | 120 |
| GAAAAGGTGG | CGGTCCCCAT | CACTCCTCCT | CTCCCATAGC | CATCCCAGAG | GGGTGAGTAG | 180 |
| CCATCANGCC | TTCGGTGGGA | GGGAGTCANG | GAAACAACAN | ACCACAGAGC | ANACAGACCA | 240 |
| NTGATGACCA | TGGGGGGGAG | CGAGCCTCTT | CCCTGNACCG | GGGTGGCANA | NGANAGCCTA | 300 |
| NCTGAGGGGT | CACACTATAA | ACGTTAACGA | CNAGATNAN  | CACCTGCTTC | AAGTGCACCC | 360 |
| TTCCTACCTG | ACNACCAGNG | ACCNNAACT  | GCNGCCTGGG | GACAGCNCTG | GGANCAGCTA | 420 |
| ACNNAGCACT | CACCTGCC   | CCCAGGGCCG | TNCGNTCCC  | TGGTCTGNC  | AAGGGAAGCT | 480 |
| CCCTGTTGGA | ATTNCGGGG  | NACCAAGGGA | NCCCCCTCCT | CCANCTGTGA | AGGAAAANN  | 540 |
| GATGGAATT  | TNCCCTTCCG | GCCNNTCCCC | TCTTCCTTTA | CACGCCCT   | NNTACTCN   | 600 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TCCCTCTNTT | NTCCTGNCNC | ACTTTNACC  | CCNNNATTTC | CCTTNATTGA | TCGGANNCTN | 660 |
| GANATTCCAC | TNNCGCCTNC | CNTCNATCNG | NAANACAAA  | NACTNTCTNA | CCCNGGGAT  | 720 |
| GGGNCCCTCG | NTCATCCTCT | CTTTTCNCT  | ACCNCCNNTT | CTTTGCCTCT | CCTTNGATCA | 780 |
| TCCAACNTC  | GNTGCCNTN  | CCCCCCCCNN | TCCTTNCCCC |            |            | 820 |

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| TCTGGGTGAT | GGCCTCTTC  | TCCTCAGGGA | CCTCTGACTG  | CTCTGGGCCA  | AAGAATCTCT | 60  |
| TGTTCTTCT  | CCGAGCCCA  | GGCAGCGGTG | ATTCAAGCCCT | GCCCCAACCTG | ATTCTGATGA | 120 |
| CTGCGGATGC | TGTGACGGAC | CCAAGGGCA  | AATAGGGTCC  | CAGGGTCCAG  | GGAGGGGCGC | 180 |
| CTGCTGAGCA | CTTCCGCCCC | TCACCCCTGC | CAGCCCCCTGC | CATGAGCTCT  | GGGCTGGGTC | 240 |
| TCCGCTCCA  | GGGTTCTGCT | CTTCCANGCA | NGCCANCAAG  | TGGCGCTGGG  | CCACACTGGC | 300 |
| TTCTTCTGC  | CCCNTCCCTG | GCTCTGANTC | TCTGTCTTCC  | TGTCTGTGC   | ANGCNCCTTG | 360 |
| GATCTCAGTT | TCCCTCNCTC | ANNGAACTCT | GTTTCTGANN  | TCTTCANTTA  | ACTNTGANTT | 420 |
| TATNACCNAN | TGGNCTGTNC | TGTCNNACTT | TAATGGGCCN  | GACCGGCTAA  | TCCCTCCCTC | 480 |
| NCTCCCTTCC | ANTTCNNNA  | ACCNNGCTNC | CNTCNTCTCC  | CCNTANCCCG  | CCNGGGANC  | 540 |
| CTCCTTGCC  | CTNACCANGG | GCCNNNACCG | CCCNTNNCTN  | GGGGGGCNNG  | GTNNCTNCNC | 600 |
| CTGNTNNCCC | CNCTCNCCNT | TNCCTCGTCC | CNNCNCGCN   | NNGCANNTTC  | NCNGTCCNN  | 660 |
| TNNCTCTCN  | NGNTCGNA   | NGNTCNCNT  | TNNNNNGNCN  | NGNTNNNTNCN | TCCCTCTCNC | 720 |
| CNNNTGNANG | TNNNTNNNNC | NCNGNNCCCC | NNNNCNNNNN  | NGGNNTNNNN  | TCTNCNCNGC | 780 |
| CCCNCCCCC  | NGNATTAAGG | CCTCCNNTCT | CCGGCCNC    |             |            | 818 |

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

|             |             |            |             |            |            |     |
|-------------|-------------|------------|-------------|------------|------------|-----|
| AGGAAGGGCG  | GAGGGATATT  | GTANGGGATT | GAGGGATAGG  | AGNATAANGG | GGGAGGTGTG | 60  |
| TCCCAACATG  | ANGGGTGNNGT | TCTCTTTGA  | ANGAGGGTTG  | NGTTTTTANN | CCNGGTGGGT | 120 |
| GATTNAACCC  | CATTGTATGG  | AGNAAAAGGN | TTTNAAGGGAT | TTTCAGGCTC | TTATCAGTAT | 180 |
| NTANATTCCCT | GTNAATCGGA  | AAATNATNTT | TCNNCNGGAA  | AATNTTGCTC | CCATCCGNAA | 240 |
| ATTNCTCCCG  | GGTAGTGCAT  | NTTNGGGGN  | CNGCANGTT   | TCCCAGGCTG | CTANAATCGT | 300 |
| ACTAAAGNTT  | NAAGTGGGAN  | TNCAAATGAA | AACCTNNCAC  | AGAGNATCCN | TACCCGACTG | 360 |
| TNNNTTNCCCT | TCGCCCTNTG  | ACTCTGCNNG | AGCCAATAC   | CCNNNGNAT  | GTCNCCNGN  | 420 |
| NNNGCGNCNC  | TGAAANNNNC  | TCGNGGCTNN | GANCATCANG  | GGGTTTCGCA | TAAAAGCNC  | 480 |
| CGTTTCNCAT  | NAAGGCACTT  | TNGCCTCATC | CAACCNCNTNG | CCCTCNCCA  | TTTNGCCGTC | 540 |
| NGGTTCNCT   | ACGCTNNTNG  | CNCCTNNNTN | GANATTTNC   | CCGCCTNGGG | NAANCCTCCT | 600 |
| GNAATGGGTÀ  | GGGNCTTNTC  | TTTTNACCN  | GNGGTNTACT  | AATCNCTNC  | ACGCNTNCTT | 660 |
| TCTCNACCCCC | CCCCCTTTTT  | CAATCCCANC | GGCNAATGGG  | GTCTCCCCNN | CGANGGGGG  | 720 |
| NNNCCCANNC  | C           |            |             |            |            | 731 |

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| ACTAGTCCAG | TGTGGTGGAA  | TTCCATTGTG | TTGGGGNCNC | TTCTATGANT | ANTNTTAGAT  | 60  |
| CGCTCANACC | TCACANCCCTC | CCNACNANGC | CTATAANGAA | NANNAATAGA | NCTGTNCNNNT | 120 |
| ATNTNTACNC | TCATANNCCCT | CNNNACCCAC | TCCCTCTTAA | CCCNTACTGT | GCCTATNGCN  | 180 |
| TNNCTANTCT | NTGCGCCTN   | CNANCCACCN | GTGGGCCNAC | CNCNNGNATT | CTCNATCTCC  | 240 |
| TCNCCATNTN | GCCTANANTA  | NGTNCATACC | CTATACTTAC | NCCAATGCTA | NNNCTAACNC  | 300 |
| TCCATNANTT | ANNNTAACCA  | CCACTGACNT | NGACTTTNC  | ATNANCTCCT | AATTTGAATC  | 360 |
| TACTCTGACT | CCACACNGCCT | ANNNATTAGC | ANCNTCCCC  | NACNATNTCT | CAACCAAATC  | 420 |
| NTCAACAACC | TATCTANCTG  | TCNCACACC  | NTTNCCCTCG | ATCCCCNNAC | AACCCCCCTC  | 480 |
| CCAAATACCC | NCCACCTGAC  | NCCTAACCCN | CACCATCCCC | GCAAGCCNAN | GGNCATTTAN  | 540 |
| CCACTGGAAT | CACNATNGGA  | NAAAAAAAAC | CCNACTCTC  | TANCNCNNAT | CTCCCTAACNA | 600 |
| AATNCTCTN  | NAATTTACTN  | NCANTNCAT  | CAANCCACN  | TGAAACNNAA | CCCCTGTTT   | 660 |
| TANATCCCTT | CTTTCGAAAA  | CCNACCCCTT | ANNNCCAAC  | CTTNGGGCC  | CCCCCNCTNC  | 720 |
| CCNAATGAAG | GNCNCCCAAT  | CNANGAAACG | NCCNTGAAAA | ANCNAGGCNA | ANANNNTCCG  | 780 |
| CANATCCTAT | CCCTTANTTN  | GGGGNCCCTT | NCCCNNGGCC | CC         |             | 822 |

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

|             |             |            |            |             |             |     |
|-------------|-------------|------------|------------|-------------|-------------|-----|
| CGGCCGCTG   | CTCTGGCACA  | TGCCTCTGA  | ATGGCATCAA | AAAGTGATGGA | CTGCCCATTG  | 60  |
| CTAGAGAAGA  | CCTTCTCTCC  | TACTGTCTT  | ATGGAGCCCT | GCAGACTGAG  | GGCTCCCCCTT | 120 |
| GTCTGCAGGA  | TTTGATGTCT  | GAAGTCGTGG | AGTGTGGCTT | GGAGTCCTC   | ATCTACATNA  | 180 |
| GCTGGAAGCC  | CTGGAGGGCC  | TCTCTCGCCA | GCCTCCCCCT | TCTCTCCACG  | CTCTCCANGG  | 240 |
| ACACCAAGGG  | CTCCAGGCG   | CCCATTATC  | CCAGNANGAC | ATGGTGTTTC  | TCCACGCGGA  | 300 |
| CCCATGGGGC  | CTGNAAGGCC  | AGGGTCTCTT | TTGACACCAT | CTCTCCCGTC  | CTGCCTGGCA  | 360 |
| GGCCGTGGGA  | TCCACTANTT  | CTANAACGGN | CGCCACCNCG | GTGGGAGCTC  | CAGTTTTGT   | 420 |
| TCCCTNTTAAT | GAAGGTTAAT  | TGCNCCTTG  | GGCTAATCAT | NGGTACAAAC  | TNTTCTCTGT  | 480 |
| GTGAAATTGT  | TTNTCCCTC   | NCNATTCCNC | NCNACATACN | AACCCGGAAN  | CATAAAAGTGT | 540 |
| TAAAGCCTGG  | GGGTNGCCCTN | NNGAATNAAC | TNAACTCAAT | TAATTGCGTT  | GGCTCATGGC  | 600 |
| CCGCTTCCCN  | TTCNGGGAAA  | CTGTCNTCCC | CTGCNTNNNT | GAATCGGCCA  | CCCCCNNGGG  | 660 |
| AAAAGCGGTT  | TGCNTTTNG   | GGGGNTCTT  | CCNCTTCCCC | CCTCNCTAAAN | CCCTNCGCCT  | 720 |
| CGGTCGTTNC  | NGGTNGCGGG  | GAANGGGNAT | NNNCTCCNC  | NAAGGGGGNG  | AGNNNGNTAT  | 780 |
| CCCCAAA     |             |            |            |             |             | 787 |

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT  | TTTTTTGGC   | GATGCTACTG | TTAATTGCA  | GGAGGTGGGG | GTGTGTGTAC | 60  |
| CATGTACCG   | GGCTATTAGA  | AGCAAGAAGG | AAGGAGGGAG | GGCAGAGCGC | CCTGCTGAGC | 120 |
| AACAAAGGAC  | TCTGCAGCC   | TTCTCTGTCT | GTCTCTGGC  | GCAGGCACAT | GGGGAGGCCT | 180 |
| CCCGCAGGGT  | GGGGGCCACC  | AGTCCAGGGG | TGGGAGCACT | ACANGGGTG  | GGAGTGGGTG | 240 |
| GTGGCTGGTN  | CNAATGGCCT  | GNCACANATC | CCTACGATT  | TTGACACCTG | GATTTCACCA | 300 |
| GGGGACCTTC  | TGTTCTCCC   | NGGNAACTTC | NTNNATCTCN | AAAGAACACA | ACTGTTCTT  | 360 |
| CNGCANTTCT  | GGCTGTTCAT  | GGAAAGCACA | GGTGTCCNAT | TTNGGCTGG  | ACTTGGTACA | 420 |
| TATGGTTCCG  | GCCCCACCTCT | CCCNTCNAAN | AAGTAATTCA | CCCCCCCCCN | CCNTCTNTTG | 480 |
| CCTGGGCCCT  | TAANTACCCA  | CACCGGAAC  | CANTTANTTA | TTCATCTTNG | GNTGGGCTTG | 540 |
| NTNATCNCN   | CCTGAANGCG  | CCAAGTGAA  | AGGCCACGCC | GTNCCCNCTC | CCCATAGNAN | 600 |
| NTTTNNCNCNT | CANCTAATGC  | CCCCCCNGC  | AACNATCAA  | TCCCCCCCN  | TGGGGGCC   | 660 |
| AGCCCANGC   | CCCCGNCTCG  | GGNNNCNGN  | CNCGNANTCC | CCAGGNTCTC | CCANTCNGNC | 720 |
| CCNNNGCNCC  | CCCGCAGC    | GAACANAAGG | NTNGAGCCNC | CGCANNNNNN | NGGTNNCNAC | 780 |
| CTCGCCCCC   | CCNCGNNG    |            |            |            |            | 799 |

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | 60  |
| TTTNCCNAG  | GGCAGGTTA  | TTGACAACCT | CNCGGACAC  | AANCAGGCTG | 120 |
| GGCAACAGGC | TCCGGCGCGG | GCGGCGGCGG | CCCTACCTGC | GGTACCAAAT | 180 |
| CGCTCCCGCT | TGATNTTCCT | CTGCAGCTGC | AGGATGCCNT | AAAACAGGGC | 240 |
| GGTGGGCACC | CTGGGATTIN | AATTCCACG  | GGCACAATGC | GGTCGCANCC | 300 |
| NATTAGGAAT | AGTGGTNTTA | CCCNCCNCCG | TTGCNCNACT | CCCCNTGGAA | 360 |
| GCGGCTCCGG | CATCTGGTCT | AAACNCTGGG | GCCCTCTTTT | TGGTTANTNT | 420 |
| NCCNGCCACA | ATCATNACTC | AGACTGGCNC | GGGCTGGCCC | AAAAAANCN  | 480 |
| GGNCCATGTC | TTNNCGGGGT | TGTCGNATN  | TNCATCACCT | CCGGGGCNCA | 540 |
| CCAAAAGTTC | TTGNGGCCCN | AAAAAANCT  | CCGGGGGNC  | CCAGTTCAA  | 600 |
| CCCTTGGCC  | CCCAAATCCT | CCCCCGNTT  | NCTGGGTTG  | GAACCCACG  | 660 |
| TGGNNGGCAA | GNTGGNTCCC | CCTCAGGGCC | CCCGGTGGC  | CCNCTCTAA  | 720 |
| NTCCTNNCA  | CCATCCCCC  | NNGNNACGNC | TANCAANGNA | TCCCTTTTT  | 780 |
| CCCCCCNCG  |            |            |            |            | 789 |

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| GACAGAACAT  | GTTGGATGGT | GGAGCACCTT | TCTATACGAC | TTACAGGACA | GCAGATGGGG | 60  |
| AATTCAATGGC | TGTTGGAGCA | ATANAACCCC | AGTTCTACGA | GCTGCTGATC | AAAGGACTTG | 120 |
| GACTAAAGTC  | TGATGAACCT | CCCAATCAGA | TGAGCATGGA | TGATTGGCCA | GAAATGAANA | 180 |
| AGAAAGTTGC  | AGATGTATT  | GCAAAGAAGA | CGAAGGCAGA | GTGGTGTCAA | ATCTTGACG  | 240 |
| GCACAGATGC  | CTGTGTGACT | CCGGTTCTGA | CTTTGAGGA  | GGTTGTTCAT | CATGATCACA | 300 |

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| ACAANGAACG | GGGCTCGTTT | ATCACCANTG  | AGGAGCAGGA | CGTGAGCCCC | CGCCCTGCAC | 360 |
| CTCTGCTGTT | AAACACCCCA | GCCATCCCTT  | CTTTCAAAAG | GGATCCACTA | CTTCTAGAGC | 420 |
| GGNCGCCACC | GCGGTGGAGC | TCCAGCTTTT  | GTTCCCTTTA | GTGAGGGTTA | ATTGCGCGCT | 480 |
| TGGCGTAATC | ATGGTCATAN | CTGTTCTGT   | TGTGAAATTG | TTATCCGCTC | ACAATTCCAC | 540 |
| ACAACATACG | ANCCGGAAGC | ATNAAATTT   | AAAGCCTGGN | GGTNGCCTAA | TGANTGAACT | 600 |
| NACTCACATT | AATTGGCTTT | GCGCTACTG   | CCCGCTTCC  | AGTCCGGAAA | ACCTGTCTT  | 660 |
| GCCAGCTGCC | NTTAATGAAT | CNGGCCACCC  | CCCAGGGAAA | AGGCNGTTG  | CTTNTTGGGG | 720 |
| CGCNCTTCCC | GCTTCTCGC  | TTCCCTGAANT | CCTTCCCCCC | GGTCTTTCGG | CTTGCAGCNA | 780 |
| ACGGTATCNA | CCT        |             |            |            |            | 793 |

## (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 756 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| GCCGCGACCG | GCATGTACGA  | GCAACTCAAG | GGCGAGTGG   | ACCGTAAAAG | CCCCAATCTT | 60  |
| ANCAAGTGCG | GGGAANAGCT  | GGGTCGACTC | AAGCTAGTT   | TTCTGGAGCT | CAACTTCTTG | 120 |
| CCAACCACAG | GGACCAAGCT  | GACCAACAG  | CAGCTAATT   | TGGCCCGTGA | CATACTGGAG | 180 |
| ATCGGGGCC  | AATGGAGCAT  | CCTACGCAAN | GACATCCCCT  | CCTCGAGCG  | CTACATGCC  | 240 |
| CAGCTCAAAT | GCTACTACTT  | TGATTACAA  | GAGCAGCTCC  | CCGAGTCAGC | CTATATGCAC | 300 |
| CAGCTCTTGG | GCCTCAACCT  | CCTCTTCTGT | CTGTCCTCAGA | ACCGGGTGGC | TGANTNCAC  | 360 |
| ACGGANTTGG | ANCGGCTGCC  | TGCCCAANGA | CATACANACC  | AATGTCTACA | TCNACCACCA | 420 |
| GTGTCTTGG  | GCAACTACTGA | TGGANGGCAG | CTACCNAAA   | GTNTTCTGG  | CCNAGGGTAA | 480 |
| CATCCCCCGC | CGAGAGCTAC  | ACCTTCTTC  | TTGACATCCT  | GCTCGACACT | ATCAGGGATG | 540 |
| AAAATCGCNG | GGTTGCTCCA  | GAAAGGCTNC | AANAANATCC  | TTTCNCTGA  | AGGCCCCCGG | 600 |
| ATNCNCTAGT | NCTAGAATCG  | GCCCCCCATC | CGCGTGGANC  | CTCCAACCTT | TCGTTNCCT  | 660 |
| TTACTGAGGG | TTNATTGCGG  | CCCTTGGCGT | TATCATGGTC  | ACNCCNGTTN | CCTGTGTTGA | 720 |
| AATTNTTAAC | CCCCCACAAT  | TCCACGCCNA | CATTNG      |            |            | 756 |

## (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 834 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

|             |             |            |             |            |            |     |
|-------------|-------------|------------|-------------|------------|------------|-----|
| GGGGATCTCT  | ANATCNACCT  | GNATGCATGG | TTGTCGGTGT  | GGTCGCTGTC | GATGAANATG | 60  |
| AACAGGATCT  | TGCCCCTTGAA | GCTCTCGCT  | GCTGTNTTTA  | AGTTGCTCAG | TCTGCCGTCA | 120 |
| TAGTCAGACA  | CNCTCTTGGG  | CAAAAAACAN | CAGGATNTGA  | GTCTTGATTT | CACCTCCAAT | 180 |
| AATCTTCNGG  | GCTGTCTGCT  | CGGTGAACTC | GATGACNANG  | GGCAGCTGGT | TGTGTNTGAT | 240 |
| AAANTCCANC  | ANGTTCTCCT  | TGGTGACCTC | CCCTTCAAAG  | TTGTTCCGGC | CTTCATCAAA | 300 |
| CTTCTNNAAAN | ANGANNANCC  | CANCTTTGTC | GAGCTGGNAT  | TTGGANAACA | CGTCACTGTT | 360 |
| GGAAACTGAT  | CCCAAATGGT  | ATGTCACTCA | TCGCCTCTGC  | TGCGCTGAAA | AAACTTGCTT | 420 |
| GGCNCAAATC  | CGACTCCCCN  | TCCTTGAAAG | AAGCCNATCA  | CACCCCCCTC | CCTGGACTCC | 480 |
| NNCAANGACT  | CTNCCGCTNC  | CCCNCCNNG  | CAGGGTTGGT  | GGCANNCCGG | GCCCNTGCGC | 540 |
| TTCTTCAGCC  | AGTTCACNAT  | NTTCATCAGC | CCCTCTGCCA  | GCTGTTNTAT | TCCTTGGGGG | 600 |
| GGAANCCGTC  | TCTCCCTTCC  | TGAANNAACT | TTGACCCTGNG | GAATAGCCGC | GCNTCNCNT  | 660 |
| ACNTNCTGGG  | CCGGGTTCAA  | ANTCCCTCCN | TTGNCCNTCN  | CCTCGGGCCA | TTCTGGATT  | 720 |
| NCNAACTTT   | TTCCTTCCCC  | CNCCCCNCGG | NGTTTGGNTT  | TTTCATNGGG | CCCCAACTCT | 780 |

GCTNTTGGCC ANTCCCCTGG GGGCNTNTAN CNCCCCCTNT GGTCCCNNTNG GGCC

834

## (2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| CGGNCGTTT   | CCNGCCGC   | CCCGTTCCA  | TGACNAAGGC  | TCCCTTCANG | TTAAATACNN | 60  |
| CCTAGNAAAC  | ATTAATGGGT | TGCTCTACTA | ATACATCATA  | CNAACCAGTA | AGCCTGCCA  | 120 |
| NAACGCCAAC  | TCAGGCCATT | CCTACCAAAG | GAAGAAAAGGC | TGGTCTCTCC | ACCCCTGTA  | 180 |
| GGAAAGGCCT  | GCCTTGTAAG | ACACCACAAT | NCGGTGAAT   | CTNAAGTCTT | GTGTTTACT  | 240 |
| AATGGAAAAA  | AAAATAAAC  | AANAGGTTT  | GTTCTCATGG  | CTGCCACCG  | CAGCCTGGCA | 300 |
| CTAAAACANC  | CCAGCGCTCA | CTTCTGCTTG | GAAAATATT   | CTTGCTCTT  | TTGGACATCA | 360 |
| GGCTTGATGG  | TATCACTGCC | ACNTTCCAC  | CCAGCTGGGC  | NCCCTTCCCC | CATNTTTGTC | 420 |
| ANTGANCTGG  | AAGGCCTGAA | NCTTAGTCTC | CAAAAGTCTC  | NGCCCACAAG | ACCGGCCACC | 480 |
| AGGGGANGTC  | NTTNCAGTG  | GATCTGCAA  | ANANTACCCN  | TATCATCANT | GAATAAAAAG | 540 |
| GCCCCCTGAAC | GANATGCTTC | CANCANCC   | TAAGACCCAT  | AATCCTNGAA | CCATGGTGC  | 600 |
| CTTCCGGTCT  | GATCCNAAAG | GAATGTTCT  | GGGTCCANT   | CCCTCCTTTG | TTNCTTACGT | 660 |
| TGTNTTGGAC  | CCNTGCTGN  | ATNACCCAN  | TGANATCCC   | NGAAGCACCC | TNCCCCGGC  | 720 |
| ATTTGANTTT  | CNTAAATTCT | CTGCCCTACN | NCTGAAGCA   | CNATTCCCTN | GGCNCCNAAN | 780 |
| GGNGAACTCA  | AGAAGGTCTN | NGAAAAACCA | CNCN        |            |            | 814 |

## (2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

|             |             |            |             |            |            |     |
|-------------|-------------|------------|-------------|------------|------------|-----|
| GCATGCTGCT  | CTTCCTCAAA  | GTTGTTCTTG | TTGCCATAAC  | AACCACCAT  | GGTAAAGCGG | 60  |
| GCGCAGTGTT  | CGCTGAAGGG  | GTTGTAGTAC | CAGCCGGGA   | TGCTCTCC   | GCAGAGTCCT | 120 |
| GTGCTCTGGCA | GGTCCACGCA  | ATGCCCTTG  | TCACTGGGA   | AATGGATGCG | CTGGAGCTCG | 180 |
| TCNAANCCAC  | TCTGTATTT   | TTCACANGCA | GCCTCCTCCG  | AAGCNTCCGG | GCAGTTGGGG | 240 |
| GTGTCGTAC   | ACTCCACTAA  | ACTGTCGATN | CANCAGCCC   | TTGCTGCAGC | GGAACTGGGT | 300 |
| GGGCTGACAG  | GTGCCAGAAC  | ACACTGGATT | GGCCTTCCA   | TGGAAGGGCC | TGGGGAAAT  | 360 |
| CNCCTNANCC  | CAAAACTGCCT | CTCAAAGGCC | ACCTTGACACA | CCCCGACAGG | CTAGAAATGC | 420 |
| ACTCTTCTTC  | CCAAAGGTAG  | TTGTTCTTGT | TGCCCAAGCA  | NCCTCCANCA | AACCAAAANC | 480 |
| TTGCAAAATC  | TGCTCCGTGG  | GGGTCACTNN | TACCAANGTT  | GGGGAAANAA | ACCCGGCNGN | 540 |
| GANCCNCTT   | GTTTGAATGC  | NAAGGNAATA | ATCCTCTGT   | CTTGCTTGGG | TGGAANAGCA | 600 |
| CAATTGAACT  | GTAAACNTTG  | GGCCGNGTTC | CNCTNNGGTG  | GTCTGAAACT | AATCACCGTC | 660 |
| ACTGGAAAAA  | GGTANGGCC   | TTCCTTGAT  | TCCCAANTT   | CCCCTNGNTT | TGGGTNNTT  | 720 |
| CTCCTCTNCC  | CTAAAATCG   | TNTTCCCCC  | CCNTANGCG   |            |            | 760 |

## (2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTTTTTTTT TTTTTTTTT TTTTTAAAAA CCCCCCTCCAT TGAATGAAAA             | 60  |
| CTTCNAAAAT TGTCCAACCC CCTCNCCAA ATNNCCATT CCGGGGGGGG GTTCAAACC    | 120 |
| CAAATTAATT TTGGANTTAA AATTAAATNT TNATTNGGGG AANAANCCAA ATGTNAAGAA | 180 |
| AATTTAACCC ATTATNAACT TAAATNCCTN GAAACCCNTG GNTTCCAAAA ATTTTAACC  | 240 |
| CTTAAATCCC TCCGAAATTG NTAANGAAA ACCAAATTCTN CCTAAGGCTN TTTGAAGGTT | 300 |
| NGATTTAACC CCCCTTNANT TNNTTTNACC CNNGNCTNAA NTATTTNGNT TCCGGTGT   | 360 |
| TCCTNTTAAN CNTNGGTAAC TCCCGNTAAT GAANNCCCT AANCCAATTA AACCGAATT   | 420 |
| TTTTGAATT GGAAATTCCN NGGAATTNA CGGGGTTTT TCCCNITGG GGGCATNCC      | 480 |
| CCCNCTTCG GGGTTGGGN NTAGGTTGAA TTTTNNANG NCCCAAAAAA NCCCCCAANA    | 540 |
| AAAAAAACTCC CAAGNNTTAA TTNGAATNTC CCCCTTCCCA GGCCTTTGG GAAAGGNGGG | 600 |
| TTNTNTGGGG CCNGGGANTT CNTTCCCCCN TTNCNCCCC CCCCCCNGGT AAANGGTTAT  | 660 |
| NGNNNTTGTT TTTGGGCC CTTNANGGAC CTTCCGGATN GAAATTAAAT CCCCGGGNCG   | 720 |
| CCCG                                                              | 724 |

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| TTTTTTTTT TTTTCTTTG CTCACATTTA ATTTTATTT TGATTTTTT TAATGCTGCA       | 60  |
| CAACACAATA TTTATTTCAT TTGTTCTTT TATTTCATTT TATTGTTTG CTGCTGCTGT     | 120 |
| TTTATTTATT TTTACTGAAA GTGAGAGGGG ACTTTGTGG CCTTTTTTCC TTTTCTGTA     | 180 |
| GGCCGCCCTA AGCTTTCTAA ATTTGGAACA TCTAAGCAAG CTGAANGAA AAGGGGGTTT    | 240 |
| CGCAAATCA CTCGGGGGAA NGGAAGGTT GCTTTGTTAA TCATGCCCTA TGGTGGGTGA     | 300 |
| TTAAGTGTGTT GTACAATTAC NTTTCACTTT TAATTAAATTG TGCTNAANGC TTTAATTANA | 360 |
| CTTGGGGGTT CCCTCCCCAN ACCAACCCCN CTGACAAAAA GTGCCNGCCC TCAAATNATG   | 420 |
| TCCCCGCNNT CNTTGAAACA CACNGCNGAA NGTTCTCATT NTCCCCNCNC CAGGTNAAAA   | 480 |
| TGAAGGGTTA CCATNTTTAA CNCCACCTCC ACNTGGCENN GCCTGAATCC TCNAAAANCN   | 540 |
| CCCTCAANCN AATTNCTNNG CCCCCTGNC GCNTNNGTCC CNCCCCGGCT CCGGGAANTN    | 600 |
| CACCCCCNGA ANNCNNNTNC NAACNAAATT CCGAAAATAT TCCCNNTCNC TCAATTCCCC   | 660 |
| CNNAGACTNT CCTCNCNNAN CNCAATTTC TTTINNTCAC GAACNCGNNC CNNAAAATGN    | 720 |
| NNNNCNCCCTC CNCTNGTCCN NAATCNCCAN C                                 | 751 |

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GTGGTATTTT CTGTAAGATC AGGTGTTCCCT CCCTCGTAGG TTTAGAGGAA ACACCCTCAT | 60  |
| AGATGAAAC CCCCCCGAGA CAGCAGCACT GCAACTGCCA AGCAGCCGG GTAGGAGGGG    | 120 |
| CGCCCTATGC ACAGCTGGGC CCTTGAGACA GCAGGGCTTC GATGTCAGGC TCGATGTCAA  | 180 |

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| TGGTCTGGAA  | GCGGCGGCTG | TACCTGCGTA | GGGGCACACC | GTCAGGGCCC  | ACCAGGAACT | 240 |
| TCTCAAAGTT  | CCAGGCAACN | TCGTTGCGAC | ACACCGGAGA | CCAGGTGATN  | AGCTTGGGT  | 300 |
| CGGTCTATAAN | CGCGGTGGCG | TCGTCGCTGG | GAGCTGGCAG | GGCCTCCCGC  | AGGAAGGCNA | 360 |
| ATAAAAGGTG  | CGCCCCCGCA | CGGTTCANCT | CGCACCTCTC | NAANACCATG  | ANGTTGGCT  | 420 |
| CNAACCCACC  | ACCANNCCGG | ACTTCCTTGA | NGGAATTCCC | AAATCTCTC   | GNTCTTGGC  | 480 |
| TTCTNCTGAT  | GCCCTANCTG | GTTGCCNGN  | ATGCCAANCA | NCCCCAANCC  | CCGGGGTCCT | 540 |
| AAANCACCCN  | CCTCCTCNNT | TCATCTGGGT | TNTNTNTCCC | GGACCNNTGGT | TCCTCTCAAG | 600 |
| GGANCCCATA  | TCTCNACCAN | TACTCACCN  | NCCCCCCNT  | GNNAACCCANC | CTTCTANNGN | 660 |
| TTCCCNCCCC  | NCCTCTGGCC | CNTCAAANAN | GCTTNACNA  | CCTGGGTCTG  | CCTTCCCCCC | 720 |
| TNCCCTATCT  | GNACCCCN   | TTTGTCTCAN | TNT        |             |            | 753 |

## (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 341 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ACTATATCCA | TCACAACAGA | CATGCTTCAT | CCCATAGACT | TCTTGACATA | GCTTCAAATG | 60  |
| AGTGAACCCA | TCCTTGATTT | ATATACATAT | ATGTTCTCAG | TATTTTGGGA | GCCCTTCAC  | 120 |
| TTCTTTAAC  | CTTGTTCATT | ATGAACACTG | AAAATAGGAA | TTTGTGAAGA | GTAAAAAAGT | 180 |
| TATAGCTTGT | TTACGTAGTA | AGTTTTGAA  | GTCTACATT  | AATCCAGACA | CTTAGTTGAG | 240 |
| TGTTAAACTG | TGATTTTAA  | AAAATATCAT | TTGAGAATAT | TCTTCAGAG  | GTATTTTCAT | 300 |
| TTTACTTTT  | TGATTAATTG | TGTTTTATAT | ATTAGGGTAG | T          |            | 341 |

## (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 101 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

|            |            |            |            |            |           |     |
|------------|------------|------------|------------|------------|-----------|-----|
| ACTTACTGAA | TTTAGTTCTG | TGCTCTTCCT | TATTTAGTGT | TGTATCATAA | ATACTTGAT | 60  |
| GTTCAAACA  | TTCTAAATAA | ATAATTTCA  | GTGGCTTCAT | A          |           | 101 |

## (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ACATCTTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCCTTCCTG GTCCCTCACCC | 60  |
| TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTTACAGC AAATTAAGAT   | 120 |
| TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAGTCT AAGAAACCCA   | 180 |
| CCTCTTGAGA GGTCAGTAA GAGGACTTAA TATTTCATAT CTACAAAATG ACCACAGGAT    | 240 |
| TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC   | 300 |
| TCGAA                                                               | 305 |

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 852 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACATAAAATAT CAGAGAAAAG TAGTCTTGA AATATTTACG TCCAGGAGTT CTTTGTCT   | 60  |
| GATTATTGG TGTGTGTTTT GGTTTGTGTC CAAAGTATTG GCAGCTTCAG TTTTCATTT   | 120 |
| CTCTCCATCC TCGGGCATTC TTCCCAAATT TATATACCAG TCTTCGTCCA TCCACACGCT | 180 |
| CCAGAATTTC TCTTTGTAG TAATATCTCA TAGCTCGGCT GAGCTTTCA TAGGTATGC    | 240 |
| TGCTGTGTT CTTCTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTC AAGAACCTGA   | 300 |
| AGACGCCCTC AGATCGGTCT TCCCATTAA TTAATCCTGG GTTCTTGCTCT GGGTCAAGA  | 360 |
| GGATGTCGCG GATGAATTCC CATAAGTGAG TCCCTCTCGG GTTGTGCTTT TTGGTGTGGC | 420 |
| ACTTGGCAGG GGGGTCTTGC TCCTTTCA TATCAGGTGA CTCTGCAACA GGAAGGTGAC   | 480 |
| TGGTGGTTGT CATGGAGATC TGAGCCCGC AGAAAGTTT GCTGTCCAAC AAATCTACTG   | 540 |
| TGCTACCATATA GTGGTGTCA TATAAAATAGT TCTNGTCTT CCAGGTGTT ATGATGGAAG | 600 |
| GCTCAGTTTG TTCAGTCTTG ACAATGACAT TGTGTGTTA CTGGAACAGG TCACTACTGC  | 660 |
| ACTGGCGTT CCACCTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCG GCCGTCCCTG  | 720 |
| CCGCCCGGT GAACTCCTGC AAACTCATGC TGCAAAGGTG CTCGCCGTT ATGTGGAACT   | 780 |
| CNTGAAAGG GATACAATTG GCATCCAGCT GTGGTGTCA CAGGAGGTGA TGGAGCCACT   | 840 |
| CCACACACTG GT                                                     | 852 |

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCG  | 60  |
| AGTCGACAC CATCCGGAGC ATCAGCATTG CTTCGCAGTG CCCTACCGCG GGGAACTCTT  | 120 |
| GCCTCGTTTC TGGCTGGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCAGTGCG | 180 |

TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT

234

## (2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 590 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| ACTTTTTATT TAAATGTTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA    | 60  |
| ATTTGATAGC AATATTTGAG AGATTACAGA GTTTTAGTAA TTACCAATTAA CACAGTTAAA   | 120 |
| AAGAAGATAAA TATATTCCAA GCANATACAA AATATCTAAAT GAAAGATCAA GGCAGGAAAAA | 180 |
| TGANTATAAC TAATTGACAA TGGAAAATCA ATTTTAATGT GAATTGCACA TTATCCTTTA    | 240 |
| AAAGCTTTCA AAANAAANAA TTATTGCACT GTANTTAATT CAAACAGTGT TAAATGGTAT    | 300 |
| CAGGATAAAAN AACTGAAGGG CANAAAAGAT TAATTTCAC TTCACTGTAAC NCACCCANAT   | 360 |
| TTACAATGGC TAAATAGCAN GGAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTTC     | 420 |
| TGGCTCTCTAA TCTGCCTTAC TCTTGGGTG TGGCTTGAT CCTCTGGAGA CAGCTGCCAG     | 480 |
| GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAG GACACATGCT     | 540 |
| GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT               | 590 |

## (2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 774 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTAAAG AAGGAAAAAA AACGAGGCC   | 60  |
| TGAACAGAAT TTCCCTGNAC AACGGGGCTT CAAAATAATT TTCTGGGGA GGTTCAAGAC  | 120 |
| GCTTCACTGC TTGAAACTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG | 180 |
| CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAG GGGACAAAGG CTAATCCAA  | 240 |
| AACATCAAAG AAAGGAAGGT GGCCTCATAC CTCCCAGCCT ACACAGTTCT CCAGGGCTCT | 300 |
| CCTCATCCCT GGAGGACGAC AGTGGAGGAA CAACTGACCA TGTCCTCAGG CCTCTGTGTG | 360 |
| CTGGCTCTG GTCTTCAGCC CCCAGCTCTG GAAGCCCACC CTCTGCTGAT CCTGCGTGGC  | 420 |
| CCACACTCCT TGAACACACA TCCCCAGTT ATATTCTGG ACATGGCTGA ACCTCCTATT   | 480 |
| CCTACTTCCG AGATGCTTG CTCCCTGCAG CCTGCAAAA TCCCACCTCAC CCTCCAAACC  | 540 |
| ACGGCATGGG AAGCCTTCT GACTTGCTG ATTACTCCAG CATCTGGAA CAATCCCTGA    | 600 |
| TTCCCCACTC CTTAGAGGCC AGATAGGGTG GTTAAGACTA GGGCTGGACC ACTTGGAGCC | 660 |
| AGGCTGCTGG CTTCAAATTN TGGCTCATTT ACGAGCTATG GGACCTTGGG CAAGTNATCT | 720 |
| TCACTTCTAT GGGCNTCATT TTGTTCTACC TGCAAAATGG GGGATAATAA TAGT       | 774 |

## (2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 124 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CANAAATTGA AATTTTATAA AAAGGCATTT TTCTCTTATA TCCATAAAAT GATATAATTT | 60  |
| TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTCCTT AATTACAGCT CAACGCAACT  | 120 |
| TGGT                                                              | 124 |

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| GCCGATGCTA CTATTTTATT GCAGGAGGTG GGGGTGTTT TATTATTCTC TCAACAGCTT | 60  |
| TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTT TACGGGTGAT TGCAAAAATT | 120 |
| TTAGGGCACC CATATCCCAA GCANTGT                                    | 147 |

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

|                                                                |     |
|----------------------------------------------------------------|-----|
| ACATTAATT ATAAGGAGGA CTGTTGGGT TCTGCTAAA CACATGGCTT GATATATTGC | 60  |
| ATGGTTGAG GTTAGGAGGA GTTAGGCATA TGTTTGGGA GAGGGGT              | 107 |

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

|            |            |     |
|------------|------------|-----|
| GTCTAGGGAA | GTCTAGGGAA | 60  |
| CACACGACTC | TGGGGTCACG | 120 |
| GGGCCGACAC | ACTTGCACGG | 180 |
| CGGGAAGGAA | AGGCAGAGAA | 204 |
| GTGACACCCT | CAGGGGGAAA |     |
| TGACAGAAAG |            |     |
| GAAAATCAAG |            |     |
| GCCTTGCAAG | GTCAGAAAGG |     |
| GGACTCAGGG | CTTCCACCAC |     |
| AGCCCTGCC  | CACTTGGCCA |     |
| CCTCCCTTTT | GGGACCAGCA |     |
| ATGT       |            |     |

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

|             |             |     |
|-------------|-------------|-----|
| ACAAAGATAAA | CATTTATCTT  | 60  |
| ATAACAAAAAA | TTTGATAGTT  | 120 |
| TTAAAGGTTA  | GTATTGTGTA  | 180 |
| GGGTATTTTC  | CAAAGACTA   | 240 |
| AAGAGATAAC  | TCAGGTAAAA  | 300 |
| AGTTAGAAAT  | GTATAAAACA  | 360 |
| CCATCAGACA  | GGTTTTAA    | 420 |
| AAACAAACATA | TTACAAAATT  | 480 |
| AGACAAATCAT | CCTTAAAAAA  | 491 |
| AAAACCTCTT  | GTATCAATT   |     |
| CTTTTGTCA   | AAATGACTGA  |     |
| CTTAANTATT  | TTTAAATATT  |     |
| TCANAAACAC  | TTCCTCAAAA  |     |
| ATTTTCAANA  | TGGTAGCTT   |     |
| CANATGTNCC  | CTCAGTCCC   |     |
| ATGTTGCTCA  | GATAAATAAA  |     |
| TCTCGTGAGA  | ACTTACCAACC |     |
| CACCACAAAGC | TTTCTGGGC   |     |
| ATGCAACAGT  | GTCTTTCTT   |     |
| TNCCTTTCT   | TTTTTTTTT   |     |
| TTACAGGCAC  | AGAAACTCAT  |     |
| CAATTATTATT | TGGATAACAA  |     |
| AGGGTCTCCA  | AATTATATTG  |     |
| AAAAATAAAT  | CCAAGTTAAT  |     |
| ATCACTCTTG  | T           |     |

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

|            |            |     |
|------------|------------|-----|
| ACATAATTAA | GCAGGGCTAA | 60  |
| TTACCATAAG | ATGCTATTAA | 120 |
| TTAANAGGTN | TATGATCTGA | 180 |
| GTATTAACAG | TTGCTGAAGT | 240 |
| TTGGTATTTT | TATGCAGCAT | 300 |
| TTCCTTITTC | TTTGATAAAC | 360 |
| ACTACAGAAC | CCTTAAGGAC | 420 |
| ACTGAAAATT | AGTAAGTAAA | 480 |
| GTTCAAAAC  | TTAAACAGTT | 484 |
| AAAAAAAAGT | AAATTTG    |     |
| GTTGAAATCT |            |     |
| GCACTAGTAT | ANACCGCTCC |     |
| TGTCAGGATA | ANACTGCTT  |     |
| GAACAGAA   | GGGAAAAANC |     |
| AGCTTGANT  | TTCCTTGTC  |     |
| TGATANGAGG | AAAGGCTGAA |     |
| TTACCTTGTT | GCCTCTCCCT |     |
| AATGATTGGC | AGGTCNGGTA |     |
| AATNCCAAA  | CATATTCCAA |     |
| CTCAACACTT | CTTTTCCNCG |     |
| TANCTTGANT | CTGTGTATTC |     |
| CAGGANCAGG | CGGATGGAAT |     |
| GGGCCAGCCC | NCGGATGTT  |     |
| CANT       |            |     |

## (2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTAACCTC GTGCTTGTA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG   | 60  |
| CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAAAACAC AAATCCTTGG CACTGGCTAG | 120 |
| TCTATGTCTT CTCAAGTGCC TTTTGTGTTG T                                | 151 |

## (2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 91 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

|                                                                   |    |
|-------------------------------------------------------------------|----|
| ACCTGGCTTG TCTCCGGGTG GTTCCCCGCG CCCCCCACGG TCCCCAGAAC GGACACTTTC | 60 |
| GCCCTCCAGT GGATACTCGA GCCAAAGTGG T                                | 91 |

## (2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 133 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGCGGATGT CGTTGGTTAT ATACAAATAT GTCATTTAT GTAAGGGACT TGAGTATACT   | 60  |
| TGGATTTTG GSTATCTGTGG GTTGGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC | 120 |
| AAGGGACAAC TGT                                                    | 133 |

## (2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 147 base pairs  
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC | 60  |
| GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA | 120 |
| TCTCANTGGG CTGGATNCAT GCAGGGT                                     | 147 |

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 198 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGTAAAATAC ATTGAATTTT CTGTATACTC | 60  |
| TGATTACATA CATTATCCT TTAAAAAAGA TGTAAATCTT AATTTTTATG CCATCTATTA  | 120 |
| ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TTAACTAGTT | 180 |
| TTGACTTCTA AGTTGGT                                                | 198 |

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 330 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACAACAAATG GGTTGTGAGG AAGTCTTATC AGCAAAACTG GTGATGGCTA CTGAAAAGAT  | 60  |
| CCATTGAAAA TTATCATTA TGATTTAAA TGACAAAGTTA TCAAAAAACTC ACTCAATTTT  | 120 |
| CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA  | 180 |
| TACAGTCAAT AAATGACAAA GCCAGGGCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG   | 240 |
| CAGAAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT | 300 |
| TTTCGTCTTT ATTGGACTTC TTTGAAGAGT                                   | 330 |

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 175 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC | 60  |
| GTCGTGGCT CTTCCCTCT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCAC     | 120 |
| TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGCG ATTCCCGTGC CTGGT      | 175 |

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 154 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACCCCACTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT   | 60  |
| GGTTGTTGCT CTTCAACAGT ATCCTCCCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC | 120 |
| TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT                              | 154 |

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

|                                  |    |
|----------------------------------|----|
| CGCTCGAGCC CTATAGTGAG TCGTATTAGA | 30 |
|----------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 89 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

|                                                                    |    |
|--------------------------------------------------------------------|----|
| ACAAAGTCATT TCAGCACCCCT TTGCTCTTCA AAACTGACCA TCTTTATAT TTAATGCTTC | 60 |
| CTGTATGAAT AAAAATGGTT ATGTCAAGT                                    | 89 |

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

|                                                                    |    |
|--------------------------------------------------------------------|----|
| ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAAATAAA GGTTCTGCAG | 60 |
| AATCAGTGCA TCCAGGATTG GTCCTTGGAT CTGGGGT                           | 97 |

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAAACCT GGAACCCCCCT TTTGATGGCA | 60  |
| GCATGGCGTC CTAGGCCTTG ACACAGCGGC TGGGGTTTGG GCTNTCCCAA ACCGCACACC  | 120 |
| CCAACCCCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT | 180 |
| TCGGTCATAA NATGAAATCC CAANGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA   | 240 |
| GGTGTGTGTT GCTCAGCCAG AAAACAGCTG CCTGGCATTC GCCGCTGAAC TATGAACCCG  | 300 |
| TGGGGGTGAA CTACCCCCAN GAGGAATCAT GCCTGGGCGA TGCAANGGTG CCAACAGGAG  | 360 |
| GGGGGGGAGG AGCATGT                                                 | 377 |

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| ACGGCCTTCC | CTCAGAATTG  | AGGGAAGAGA | CTGTCGCCTG | CCTTCCTCCG  | TTGTTGCGTG | 60  |
| AGAACCCGTG | TGCCCTTC    | CACCATATCC | ACCCTCGCTC | CATCTTGAA   | CTCAAACACG | 120 |
| AGGAACTAAC | TGCACCCCTGG | TCCTCTCCCC | AGTCCCCAGT | TCACCCCTCCA | TCCCTCACCT | 180 |
| TCCTCCACTC | TAAGGGATAT  | CAACACTGCC | CAGCACAGGG | GCCCCTGAATT | TATGTGGTTT | 240 |
| TTATATATTT | TTAATAAGA   | TGCACTTAT  | GTCATTTTT  | AATAAAGTCT  | GAAGAATTAC | 300 |
| TGTTT      |             |            |            |             |            | 305 |

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ACTACACACA | CTCCACTTGC | CCTTGTGAGA | CACTTTGTCC | CAGCACTTTA | GGAATGCTGA | 60  |
| GGTGGGACCA | GCCACATCTC | ATGTGCAAGA | TTGCCAGCA  | GACATCAGGT | CTGAGAGTTC | 120 |
| CCCTTTAAA  | AAAGGGGACT | TGCTTAAAAA | AGAAGTCTAG | CCACGATTGT | GTAGAGCAGC | 180 |
| TGTGCTGTGC | TGGAGATTCA | CTTTGAGAG  | AGTTCTCCTC | TGAGACCTGA | TCTTAGAGG  | 240 |
| CTGGGCAGTC | TTGCACATGA | GATGGGGCTG | GTCTGATCTC | AGCACTCCTT | AGTCTGCTTG | 300 |
| CCTCTCCCAG | GGCCCCAGCC | TGGCCACACC | TGTTACAGG  | GCACTCTCAG | ATGCCCATAC | 360 |
| CATAGTTTCT | GTGCTAGTGG | ACCGT      |            |            |            | 385 |

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

|            |            |           |            |            |            |    |
|------------|------------|-----------|------------|------------|------------|----|
| ACTTAACCAG | ATATATTTTT | ACCCAGATG | GGGATATTCT | TTGTAAAAAA | TGAAAATAAA | 60 |
| GTTTTTTAA  | TGG        |           |            |            |            | 73 |

## (2) INFORMATION FOR SEQ ID NO:69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

## (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

|                                                               |            |     |
|---------------------------------------------------------------|------------|-----|
| ACTAGTCCAG TGTGGTGGAA TTCCATTGTC TTGGGGGCTC TCACCCCTCCT       | CTCCTGCAGC | 60  |
| TCCAGCTTTG TGCTCTGCCT CTGAGGAGAC CATGCCAG CATCTGAGTA          | CCCTGCTGCT | 120 |
| CCTGCTGGCC ACCCTAGCTG TGGCCCTGGC CTGGAGCCCC AAGGAGGAGG        | ATAGGATAAT | 180 |
| CCCAGGTGGC ATCTATAACC CAGACCTCAA TGATGAGTGG GTACAGCGTG        | CCCTTCACCT | 240 |
| CGCCATCAGC GAGTATAACA AGGCCACCAA AGATGACTAC TACAGACGTC        | CGCTGCGGGT | 300 |
| ACTAAGAGCC AGGCAACAGA CCGTTGGGG GGTGAATTAC TTCTTCGACG         | TAGAGGTGGG | 360 |
| CCGAACCAT A TGTACCAAGT CCCAGCCAA CTTGGACACC TGTGCCCTCC        | ATGAACAGCC | 420 |
| AGAACTGCAG AAGAACAGT TGTGCTCTT CGAGATCTAC GAAGTCCCT GGGGAGAAC | A          | 480 |
| GAANGTCCCT GGGTGAAATC CAGGTGTCAA GAAATCCTAN GGATCTGTTG CCAGGC |            | 536 |

## (2) INFORMATION FOR SEQ ID NO:70:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATGACCCCTA ACAGGGGCC TCTCAGCCCT CCTAATGACC TCCGGCCTAG CCATGTGATT  | 60  |
| TCACTTCCAC TCCATAACGC TCCTCATACT AGGCCTACTA ACCAACACAC TAACCATATA | 120 |
| CCAATGATGG CGCGATGTAA CACGAGAAAG CACATACCAA GGCCACCACA CACCACCTGT | 180 |
| CCAAAAAGGC CTTCGATACC GGATAATCCT ATTATTACCC TCAGAAGTTT TTTTCTTCGC | 240 |
| AGGGATTTT CTGAGCCTTT TACCACTCCA GCCTAGCCCC TACCCCCCAA CTAGGAGGGC  | 300 |
| ACTGGCCCCC AACAGGCATC ACCCGCTAA ATCCCTAGA AGTCCCCTC CTAAACACAT    | 360 |
| CCGTATTACT CGCATCAGGA GTATCAATCA CCTGAGCTCA CCATAGTCTA ATAGAAAACA | 420 |
| ACCGAAACCA AATTATTCAA AGCACTGCTT ATTACAATTT TACTGGGTCT CTATTTT    | 477 |

## (2) INFORMATION FOR SEQ ID NO:71:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| AGAGCTATAG GTACAGTGTG ATCTCAGCTT TGCAAACACA TTTTCTACAT AGATAGTACT  | 60  |
| AGGTATTAAT AGATATGTAA AGAAAGAAAT CACACCATTA ATAATGGTAA GATTGGTTA   | 120 |
| TGTGATTTA GTGGTATTTT TGGCACCCCTT ATATATGTTT TCCAAACCTT CAGCAGTGT   | 180 |
| ATTATTCGA TAACTTAAAA AGTAGGTTG AAAAGAAAA TCTCCAGCAA GCATCTCATT     | 240 |
| TAAATAAAGG TTTGTATCT TTAAAAATAC AGCAATATGT GACTTTTAA AAAAGCTGTC    | 300 |
| AAATAGGTGT GACCCCTACTA ATAATTATTA GAAATACATT TAAACACATC GAGTACCTCA | 360 |
| AGTCAGTTG CCTTGAAAAA TATCAAATAT AACTCTTGA GAAATGTACA TAAAAGAATG    | 420 |
| CTTCGTAATT TTGGAGTANG AGGTTCCCTC CTCAATTGTTG TATTTTAAA AAGTACATGG  | 480 |

TAAAAAAAAA AATTCAACAC AGTATATAAG GCTGTAAAT GAAGAATTCT GCC

533

## (2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 511 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| TATTACGGAA | AAACACACCA | CATAATTCAA | CTANCAAAGA | ANACTGCTTC | AGGGCGTGTA  | 60  |
| AAATGAAAGG | CTTCCAGGCC | GTTATCTGAT | TAAAGAACAC | TAAAAGAGGG | ACAAGGCTAA  | 120 |
| AAGCCGCAGG | ATGTCACAC  | TATANCAGGC | GCTATTGGS  | TTGGCTGGAG | GAGCTGTGGA  | 180 |
| AAACATGGAN | AGATTGGTGC | TGGANATCGC | CGTGGCTATT | CCTCATTGTT | ATTACANAGT  | 240 |
| GAGGTTCT   | GTGTGCCAC  | TGGTTGAAA  | ACCGTTCTNC | AATAATGATA | GAATAGTACA  | 300 |
| CACATGAGAA | CTGAAATGGC | CCAAACCCAG | AAAGAAAGCC | CAACTAGATC | CTCAGAAANAC | 360 |
| GCTCTAGGG  | ACAATAACCG | ATGAAGAAAA | GATGGCCTCC | TTGTGCCCTC | GTCTGTTATG  | 420 |
| ATTCTCTCC  | ATTGCAGCNA | NAAACCCGT  | CTTCTAAGCA | AACNCAGGTG | ATGATGGCNA  | 480 |
| AAATACACCC | CCTCTTGAAG | NACCNGGAGG | A          |            |             | 511 |

## (2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 499 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

|            |             |             |            |            |             |     |
|------------|-------------|-------------|------------|------------|-------------|-----|
| CAGTGCCAGC | ACTGGTCCA   | GTACCAAGTAC | CAATAACAGT | GCCAGTGCCA | GTGCCAGCAC  | 60  |
| CAGTGGTGGC | TTCAGTCTG   | GTGCCAGCCT  | GACGCCACT  | CTCACATTG  | GGCTCTTCGC  | 120 |
| TGGCTTGGT  | GGAGCTGGTG  | CCAGCACCG   | TGGCAGCTCT | GGTGCCTGTG | GTTTCTCCCTA | 180 |
| CAAGTGAGAT | TTTAGATATT  | GTAACTCTG   | CCAGCTTTG  | TCTTCAAGCC | AGGGTGACATC | 240 |
| CTCAGAAACC | TACTAACAC   | AGCACTCTAG  | GCAGCCACTA | TCAATCAATT | GAAGTTGACA  | 300 |
| CTCTGCATTA | AATCTATTG   | CCATTCTGA   | AAAAAAAAAA | AAAAAAAGGG | CGGCCGCTCG  | 360 |
| ANTCTAGAGG | GCCC GTTTAA | ACCCGCTGAT  | CAGCCTCGAC | TGTGCCTTCT | ANTTGCCAGC  | 420 |
| CATCTGTTGT | TTGCCCTCC   | CCCGNTGCCT  | TCCTTGACCC | TGGAAAGTGC | CACTCCACT   | 480 |
| GTCCTTCCT  | AANTAAAT    |             |            |            |             | 499 |

## (2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 537 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TTTCATAGGA | GAACACACTG | AGGAGATACT | TGAAGAATT  | GGATTCAGCC | GCGAAGAGAT | 60  |
| TTATCAGCTT | AACTCAGATA | AAATCATTGA | AAGTAATAAG | GTAAAAGCTA | GTCTCTAACT | 120 |
| TCCAGGCCCA | CGGCTCAAGT | GAATTTGAAT | ACTGCATT   | CAGTGTAGAG | TAACACATAA | 180 |
| CATTGTATGC | ATGGAAACAT | GGAGGAACAG | TATTACAGTG | TCCTACCAC  | CTAATCAAGA | 240 |
| AAAGAATTAC | AGACTCTGAT | TCTACAGTGA | TGATTGAATT | CTAAAAATGG | TAATCATTAG | 300 |
| GGCTTTGAT  | TTATAANACT | TTGGGTACTT | ATACTAAATT | ATGGTAGTTA | TACTGCCCTC | 360 |
| CAGTTGCTT  | GATATATTG  | TTGATATTAA | GATTCTGAC  | TTATATTTC  | AATGGGTTCT | 420 |
| ACTGAAAAN  | GAATGATATA | TTCTTGAGA  | CATCGATATA | CATTTATTTA | CACTCTTGAT | 480 |
| TCTACAATGT | AGAAAATGAA | GGAAATGCC  | CAAATTGTAT | GGTGATAAAA | GTCCCGT    | 537 |

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 467 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| CAAANACAAT  | TGTTCAAAAG | ATGCAAATGA | TACACTACTG | CTGCAGCTCA | CAAACACCTC | 60  |
| TGCATATTAC  | ACGTACCTCC | TCCTGCTCCT | CAAGTAGTGT | GGTCTATTTT | GCCATCATCA | 120 |
| CCTGCTGTCT  | GCTTAGAAGA | ACGGCTTCT  | GCTGCAANGG | AGAGAAATCA | TAACAGACGG | 180 |
| TGGCACAAAGG | AGGCCATCTT | TTCCTCATCG | GTTATTGTCC | CTAGAAGCGT | CTTCTGAGGA | 240 |
| TCTAGTTGGG  | CTTCTTTCT  | GGGTTGGG   | CATTTCANTT | CTCATGTGTG | TACTATTCTA | 300 |
| TCATTATTGT  | ATAACGGTTT | TCAAACCN   | GGGCACNCAG | AGAACCTCAC | TCTGTAATAA | 360 |
| CAATGAGGAA  | TAGCCACGGT | GATCTCCAGC | ACCAAATCTC | TCCATGTTNT | TCCAGAGCTC | 420 |
| CTCCAGCCAA  | CCCAAATAGC | CGCTGCTATN | GTGTAGAAC  | TCCCTGN    |            | 467 |

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| AAGCTGACAG | CATTGGGCC  | GAGATGTCTC | GCTCCGTGGC | CTTAGCTGTG | CTCGCGCTAC | 60  |
| TCTCTCTTTC | TGGCCTGGAG | GCTATCCAGC | GTACTCCAAA | GATTCAAGTT | TACTCACGTC | 120 |
| ATCCAGCAGA | GAATGGAAAG | TCAAATTCC  | TGAATTGCTA | TGTGTCTGG  | TTTCATCCAT | 180 |
| CCGACATTGA | AGTTGACTTA | CTGAAGAATG | GAGAGAGAAT | TGAAAAAGTG | GAGCATTGAG | 240 |
| ACTTGTCTTT | CAGCAAGGAC | TGGCTTTCT  | ATCTCTTGTA | CTACACTGAA | TTCACCCCCA | 300 |
| CTGAAAAAGA | TGAGTATGCC | TGCCGTGTGA | ACCATGTGAC | TTTGTACAG  | CCCAAGATNG | 360 |

TTNAGTGGGA TCGANACATG TAAGCAGCAN CATGGGAGGT

400

## (2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 248 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| CTGGAGTGCC TTGGTGTTC AAGCCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT  | 60  |
| CCAGCTGCC CGGCGGGGGA TGCGAGGCTC GGAGCACCCCT TGCCCCGGCTG TGATTGCTGC | 120 |
| CAGGCACTGT TCATCTCAGC TTTTCTGTC CTTTGTCCC GGCAAGCGCT TCTGCTGAAA    | 180 |
| GTTCATATCT GGAGCCTGAT GTCTTAACGA ATAAAGGTCC CATGCTCCAC CCGAAAAAAA  | 240 |
| AAAAAAAAA                                                          | 248 |

## (2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 201 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCAA CACAATGGCT ACCTTTAAC  | 60  |
| TCACCCAGAC CCCGCCCTGC CCGTCCCCA CGCTGCTGCT AACGACAGTA TGATGCTTAC | 120 |
| TCTGCTACTC GGAAACTATT TTTATGTAAT TAATGTATGC TTTCTGTTT ATAAATGCCT | 180 |
| GATTAAAAAA AAAAAAAA A                                            | 201 |

## (2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 552 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TCCTTTGTT AGGTTTTGAA GACAACCTA GACCTAAACT GTGTCACAGA CTTCTGAATG    | 60  |
| TTTAGGCAGT GCTAGTAATT CCCTCGTAAT GATTCTGTTA TTACTTTCCCT ATTCTTTATT | 120 |
| CCTCTTCTT CTGAAGATTA ATGAAGTTGA AAATTGAGGT GGATAAAATAC AAAAAGGTAG  | 180 |

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| TGTGATAGTA TAAGTATCTA AGTCAGATG AAAGTGTGTT ATATATATCC ATTCAAAATT    | 240 |
| ATGCAAGTTA GTAATTACTC AGGGTTAAGT AAATTACTTT AATATGCTGT TGAACCTACT   | 300 |
| CTGTTCTTG GCTAGAAAAA ATTATAAACCA GGACTTTGTT AGTTGGGAA GCCAAATTGA    | 360 |
| TAATATTCTA TGTTCTAAAAA GTTGGGCTAT ACATAAANTTA TNAAGAAATA TGGAATTTTA | 420 |
| TTCCCAGGAA TATGGGGTTC ATTTATGAAT ANTACCCGGG ANAGAAGTTT TGANTNAAAC   | 480 |
| CNGTTTGTT TAATACGTTA ATATGTCCTN AATNAACAAG GCNTGACTTA TTICCAAAAA    | 540 |
| AAAAAAAAAA AA                                                       | 552 |

## (2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 476 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACAGGGATTT GAGATGCTAA GGCCCCAGAG ATCGTTGAT CCAACCCTCT TATTTTCAGA  | 60  |
| GGGGAAAATG GGGCCTAGAA GTTACAGAGC ATCTAGCTGG TCGCTGGCA CCCCTGGCCT  | 120 |
| CACACAGACT CCCGAGTAGC TGGGACTACA GGCACACAGT CACTGAAGCA GGCCCTGTTT | 180 |
| GCAATTACAG TTGCCACCTC CAACTTAAAC ATTCTTCATA TGTGATGTCC TTAGTCACTA | 240 |
| AGGTAAACT TTCCCACCCA GAAAAGGCAA CTTAGATAAA ATCTTAGAGT ACTTCATAC   | 300 |
| TCTTCTAACT CCTCTTCCAG CCTCACTTG AGTCCTCCTT GGGGGTTGAT AGGAANTNTC  | 360 |
| TCTTGGCTTT CTCAATAAAA TCTCTATCCA TCTCATGTTT AATTGGTAC GCNTAAAAAT  | 420 |
| GCTGAAAAAA TTAAAATGTT CTGGTTTNC TTTAAAAAAA AAAAAAAAAA AAAAAAA     | 476 |

## (2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 232 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| TTTTTTTTTG TATGCCNTCM CTGTGGNGTT ATTGGTGCTG CCACCCCTGGA GGAGCCCAGT  | 60  |
| TTCTTCTGTA TCTTTCTTT CTGGGGATC TTCCTGGCTC TGCCCTCTCA TTCCCAGCCT     | 120 |
| CTCATCCCCA TCTTGCACCTT TTGCTAGGGT TGGAGGGCGCT TTCCTGGTAG CCCCTCAGAG | 180 |
| ACTCAGTCAG CGGGAATAAQ TCCTAGGGGT GGGGGGTG TG GCAAGCCGGC CT          | 232 |

## (2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

|                        |                       |                       |     |
|------------------------|-----------------------|-----------------------|-----|
| AGGGGGGAGC AGAACGCTAAA | GCCAAAGCCC AAGAACAGTG | GCAGTGCCAG CACTGGTGCC | 60  |
| AGTACCAAGTA CCAATAACAT | GCCAGTGCCA GTGCCAGCAC | CAGTGGTGGC TTCAGTGCTG | 120 |
| GTGCCAGCCT GACCGCCACT  | CTCACATTG GGCTCTCGC   | TGGCCTTGGT GGAGCTGGTG | 180 |
| CCAGCACCAG TGGCAGCTCT  | GGTCAGCTGTG           | TTTCTCCTA CAAGTGAGAT  | 240 |
| GTAAATCCTG CCAGTCTTTC  | TCTTCAAGCC AGGGTGCATC | CTCAGAAACC TACTCAACAC | 300 |
| AGCACTCTNG GCAGCCACTA  | TCAATCAATT GAAGTTGACA | CTCTGCATTA AATCTATTTG | 360 |
| CCATTTCAAA             | AAAAAAAAAA AAA        |                       | 383 |

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

|                                  |                       |                         |     |
|----------------------------------|-----------------------|-------------------------|-----|
| ACCGAATTGG GACCGCTGGC TTATAAGCGA | TCATGTCCTC CAGTATTACC | TCAACGAGCA              | 60  |
| GGGAGATCGA GTCTATACGG            | TGAAGAAATT TGACCCGATG | GGACAACAGA CCTGCTCAGC   | 120 |
| CCATCCCTGCT CGGTTCTCCC           | CAGATGACAA ATACTCTCGA | CACCGAATCA CCATCAAGAA   | 180 |
| ACGCTTCAAG GTGCTCATGA            | CCCAGCAACC GCGCCCTGTC | CTCTGAGGGT CCTTAAACTG   | 240 |
| ATGTCTTTTC TGCCACCTGT            | TACCCCTCGG AGACTCCGTA | ACCAAACCTCT TC GGACTGTG | 300 |
| AGCCCTGATG CCTTTTTGCG            | AGCCATACTC TTTGGCNTCC | AGTCTCTCGT GGC GATTGAT  | 360 |
| TATGCTTG TGAGGCAATC              | ATGGTGGCAT CACCATNAA  | GGGAACACAT TTGANTTTT    | 420 |
| TTTCNCATAT TTTAAATTAC            | NACCAGAATA NTTCAAGATA | AATGAATTGA AAAACTCTTA   | 480 |
| AAAAAAAAAA AAAA                  |                       |                         | 494 |

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

|                        |                        |                        |     |
|------------------------|------------------------|------------------------|-----|
| GCTGGTAGCC TATGGCGTGG  | CCACGGGANGG GCTCCTGAGG | CACGGGACAG TGACTTCCA   | 60  |
| AGTATCCTGC GCCCGCTTCT  | CTACCGTCCC TACCTGCAGA  | TCTTCGGGCA GATTCCCCAG  | 120 |
| GAGGACATGG ACCTGGCCCT  | CATGGAGCAC AGCAACTGCT  | CGTCGGAGCC CGGCTTCTGG  | 180 |
| GCACACCCCTC CTGGGGCCCA | GGCGGGCACC TGCGCTCCC   | AGTATGCCAA CTGGCTGGTG  | 240 |
| GTGCTGCTCC TCGTCATCTT  | CCTGCTCGTG             | GCCAAACATCC TGCTGGTCAC | 300 |
| CCATGTTCAAG TTACACATTC | GGCAAAGTAC AGGGCAACAG  | CNATCTCTAC TGGGAAGGCC  | 360 |
| AGCGTTNCCG CCTCATCCGG  |                        |                        | 380 |

## (2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 481 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

|            |             |             |             |             |             |     |
|------------|-------------|-------------|-------------|-------------|-------------|-----|
| GAGTTAGCTC | CTCCACAACC  | TTGATGAGGT  | CGTCTGCAGT  | GGCCTCTCGC  | TTCATACCGC  | 60  |
| TNCCATCGTC | ATACTGTAGG  | TTGCCACCA   | CCTCCCTGCAT | CTTGGGGCGG  | CTAATATCCA  | 120 |
| GGAAACTCTC | AATCAAGTCA  | CCGTCNATNA  | AACCTGTGGC  | TGTTTCTGTC  | TTCCGCTCGG  | 180 |
| TGTGAAAGGA | TCTCCAGAAG  | GAGTGCTCGA  | TCTTCCCAC   | ACTTTTGATG  | ACTTTATTGA  | 240 |
| GTCGATTCTG | CATGTCCAGC  | AGGAGGTGT   | ACCAAGCTCTC | TGACAGTGAG  | GTCACCAGCC  | 300 |
| CTATCATGCC | TTGAAACGTC  | CCGAAGAACAA | CCGAGCCTTG  | TGTGGGGGGT  | GNAGTCTCAC  | 360 |
| CCAGATTCTG | CATTACCCAGA | NAGCCGTGGC  | AAAAGANATT  | GACAACCTCGC | CCAGGNNNGAA | 420 |
| AAAGAACACC | TCCTGGAACT  | GCTNGCCGCT  | CCTCGTCCTT  | TGGTGGNNNGC | GCNTNCCTTT  | 480 |
| T          |             |             |             |             |             | 481 |

## (2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 472 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

|             |             |            |             |             |             |     |
|-------------|-------------|------------|-------------|-------------|-------------|-----|
| AACATCTTCC  | TGTATAATGC  | TGTGTAATAT | CGATCCGATN  | TTGTCCTGCTG | AGAATTCAATT | 60  |
| ACTTGGAAAA  | GCAACTTNAA  | GCCTGGACAC | TGGTATTAAA  | ATTCAACAATA | TGCAACACTT  | 120 |
| TAAACAGTGT  | GTCAAATCTGC | TCCCTTACTT | TGTCATCACC  | AGTCTGGGAA  | TAAGGGTATG  | 180 |
| CCCTATTCAAC | ACCTGTAAA   | AGGGCGCTAA | GCATTTTGAA  | TTCACACATCT | TTTTTTTTGA  | 240 |
| CACAAGTCCG  | AAAAAAGCAA  | AAGTAAACAG | TTNTTAATTTC | GTAGCCAAT   | TCACTTTCTT  | 300 |
| CATGGGACAG  | AGCCATTGAA  | AAATTGCAAA | ATATTGAGCT  | TTGGGAGCTG  | 360         |     |
| ATATNTGAGC  | GGAAGANTAG  | CCTTTCTACT | TCACCAAGACA | CAACTCCTTT  | CATATTGGGA  | 420 |
| TGTTNACNAA  | AGTTATGTCT  | CTTACAGATG | GGATGCTTT   | GTGGCAATTG  | TG          | 472 |

## (2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 413 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

## (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGAAACCGT ATCTCTNAAA ACAACCTCTC ATACCTGTG GACCTAATT TGTGTGCGTG    | 60  |
| TGTGTGCG CGCATATTAT ATAGACAGGC ACATCTTTT TACTTTGTAAAGCTTATG       | 120 |
| CCTCTTGGT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT  | 180 |
| TTGTCTCTG TGTAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT   | 240 |
| TTTATTGAC ATGAAGGAAA TTTCCAGATN ACAACACTNA CAAACTCTCC CTTGACTAGG  | 300 |
| GGGGACAAAG AAAAGCANAA CTGAACATNA GAAACAATTN CCTGGTGAGA AATTNCATAA | 360 |
| ACAGAAATTG GGTNGTATAT TGAAANANNG CATCATTNAACGTTTTTT TTT           | 413 |

## (2) INFORMATION FOR SEQ ID NO:88:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| CGCACGGGGT CCTCTCTATC TAGCTCCAGC CTCTCGCCTG CCCCACCTCCC CGCGTCCCCGC  | 60  |
| GTCCTAGCCN ACCATGGCCG GGCCCCCTGCG CGCCCCGCGTGCCTCGCTGG CCATCCTGGC    | 120 |
| CGTGGCCCTG GCCGTGAGCC CCGCGGCCGG CTCCAGTCCC GGCAAGCCGC CGCGCCTGGT    | 180 |
| GGGAGGCCCA TGGACCCCGC GTGGAAGAAC AGGTGTGCG GCGTGCACTG GACTTTGCCG     | 240 |
| TCGGCNANTAA CAACAAACCC GCAACNACTT TTACCNAGCN CGCGCTGCAG GTTGTGCCGC   | 300 |
| CCCAANCAAA TTGTTACTNG GGGTAANTAA TTCTTGGAAAG TTGAACCTGG GCCAAACNNG   | 360 |
| TTTACCAAGAA CCNAGCCAAT TNAGAACATT NCCCCCTCCAT AACAGCCCCCT TTTAAAAAGG | 420 |
| GAANCANTCC TGNTCTTTTC CAAATTAA                                       | 448 |

## (2) INFORMATION FOR SEQ ID NO:89:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GAATTTGTG CACTGGCCAC TGTGATGGAA CCATTGGGCC AGGATGCTTT GAGTTTATCA  | 60  |
| GTAGTGATTC TGCCAAAGTT GGTGTTGTA CATGAGTATG TAAAATGTCA AAAAATTAGC  | 120 |
| AGAGGTCTAG GTCTGCATAT CAGCAGACAG TTTGTCCGTG TATTTTGATG CCTTGAAGTT | 180 |
| CTCACTGACA AGTTNNNTCT GATGCGAAGT TCTNATTCCA GTGTTTTAGT CCTTTGCATC | 240 |
| TTTNTATGTTN AGACTTGCCT CTNTAAATT GCTTTGTNT TCTGCAGGTA CTATCTGTGG  | 300 |
| TTTAACAAAA TAGAANNACT TCTCTGTTN GAANATTGA ATATCTTACA TCTNAAAATN   | 360 |
| AATTCTCTCC CCATANNAAA ACCCANGCCC TTGGGANAAT TTGAAAANG GNTCCTTCNN  | 420 |
| AATTCNNANA ANTCAGNTN TCATACAACA NAACNGGANC CCC                    | 463 |

## (2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| AGGGATTGAA | GGTCTNTNT  | ACTGTCGGAC | TGTTCANCCA  | CCAACTCTAC  | AAGTTGCTGT | 60  |
| CTTCCACTCA | CTGTCTGTAA | GCNTNTAAC  | CCAGACTGTA  | TCTTCATATAA | TAGAACAAAT | 120 |
| TCTTCACCAG | TCACATCTTC | TAGGACCTTT | TTGGATTCAAG | TTAGTATAAG  | CTCTTCCACT | 180 |
| TCCTTGTTA  | AGACTTCATC | TGGTAAAGTC | TTAAGTTTTG  | TAGAAAGGAA  | TTTAATTGCT | 240 |
| CGTTCTCTAA | CAATGTCCTC | TCCITGAAGT | ATTTGGCTGA  | ACAACCCACC  | TNAAGTCCT  | 300 |
| TTGTGCATCC | ATTTAAATA  | TACTTAATAG | GGCATGGTN   | CACTAGGTTA  | AATTCTGCCA | 360 |
| GAGTCATCTG | TCTGCAAAAG | TTGCGTTAGT | ATATCTGCCA  |             |            | 400 |

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 480 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| GAGCTCGGAT | CCAATAATCT  | TTGTCTGAGG | GCAGCACACA | TATNCAGTGC | CATGGNAACT  | 60  |
| GGTCTACCCC | ACATGGGAGC  | AGCATGCCGT | AGNTATATAA | GGTCATTCCC | TGAGTCAGAC  | 120 |
| ATGCTCTTT  | GAECTACCGTG | TGCCAGTGCT | GGTGATTCTC | ACACACCTCC | NNCCGCTCTT  | 180 |
| TGTGGAAAAA | CTGGCACTTG  | NCTGGAACTA | GCAAGACATC | ACTTACAAAT | TCACCCACGA  | 240 |
| GACACTTGAA | AGGTGTAACA  | AAGCGACTCT | TGCATTGCTT | TTTGTCCCTC | CGGCACCAAGT | 300 |
| TGTCAATACT | AACCCGCTGG  | TTTGCCTCCA | TCACATITGT | GATCTGTAGC | TCTGGATACA  | 360 |
| TCTCCTGACA | GTACTGAAGA  | ACTTCTCTT  | TTGTTTCAA  | AGCAACTCTT | GGTGCCTGTT  | 420 |
| NGATCAGGTT | CCCATTTCCC  | AGTCCGAATG | TTCACATGGC | ATATNTTACT | TCCCACAAAA  | 480 |

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 477 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ATACAGCCCCA NATCCCACCA CGAAGATGCG CTTGTTGACT GAGAACCTGA TGCAGTCAC  | 60  |
| GGTCCCGCTG TAGCCCCAGC GACTCTCCAC CTGCTGGAAG CGGTTGATGC TGCACTCCTT  | 120 |
| CCCACGCAGG CAGCAGCGGG GCCGGTCAAT GAACTCCACT CGTGGCTTG GGTTGACGGT   | 180 |
| TAANTGCAGG AAGAGGCTGA CCACCTCGCG GTCCACCAGG ATGCCCGACT GTGCGGGACC  | 240 |
| TGCAGCGAAA CCTCTCGATG GTCATGAGCG GGAAGCGAAT GANGCCCAGG GCCTTGCCCA  | 300 |
| GAACCTTCCG CTCGTTCTCT GGCCTCACCT GCAGCTGCTG CCGCTNACAC TCGGCCTCGG  | 360 |
| ACCAAGCGGAC AAACGGCGTT GAACAGCCGC ACCTCACCGA TGCCCANTGT GTCGCGCTCC | 420 |
| AGGAACGGCN CCAGCGTGTGTC CAGGTCAATG TCGGTGAANC CTCCGCGGGT AATGGCG   | 477 |

## (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 377 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GAACGGCTGG ACCTTGCCTC GCATTGTGCT GCTGGCAGGA ATACCTTGGC AAGCAGCTCC  | 60  |
| AGTCGGAGCA GCCCCAGACC GCTGCCGCC GAAAGCTAACG CTGCCTCTGG CCTTCCCCCTC | 120 |
| CGCCTCAATG CAGAACCCANT AGTGGGAGCA CTGTGTTTAG AGTTAAGAGT GAACACTGTN | 180 |
| TGATTTTACT TGGGAATTTC CTCTGTATA TAGCTTTCC CAATGCTAAT TTCCAAACAA    | 240 |
| CAACAAACAAA ATAACATGTT TGCCTGTTNA GTTGATAAAA AGTANGTGTATCTGTATNTA  | 300 |
| AAGAAAATAT TACTGTTACA TATACTGCTT GCAANTTCTG TATTTTATTGG TNCTCTGGAA | 360 |
| ATAAAATATAT TATTAAA                                                | 377 |

## (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 495 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| CCCTTTGAGG GTTGTAGGGTC CAGTTCCCAG TGGAAAGAAC AGGCCAGGAG AANTGCGTGC  | 60  |
| CGAGCTGANG CAGATTTCCC ACAGTGACCC CAGAGCCCTG GGCTATAGTC TCTGACCCCT   | 120 |
| CCAAGGAAAG ACCACCTTCT GGGGACATGG GCTGGAGGGC AGGACCTAGA GGCACCAAGG   | 180 |
| GAAGCCCCCA TTCCGGGGCT GTTCCCCGAG GAGGAAGGGGA AGGGGCTCTG TGTCCCCCCC  | 240 |
| ACGAGGAANA GGCCCTGANT CCTGGGATCA NACACCCCTT CACGTGTATC CCCACACAAA   | 300 |
| TGCAAGCTCA CCAAGGTCCC CTCTCAGTCC CTTCCCTACA CCCTGAAACGG NCACTGGCCC  | 360 |
| ACACCCACCC AGANCANCCA CCCGCCATGG GGAATGTNCT CAAGGAATCG CNGGGCAACG   | 420 |
| TGGACTCTNG TCCCNNAAAGG GGGCAGAATC TCCAATAGAN GGANNGAACCC CTTGCTNANA | 480 |
| AAAAAAAANA AAAAAA                                                   | 495 |

## (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| GGTTACTTGG | TTTCATTGCC | ACCACTTAGT | GGATGTCATT | TAGAACCAATT | TTGTCTGCTC | 60  |
| CCTCTGGAAG | CCTTGCGCAG | AGCGGACTTT | GTAATTGTTG | GAGAATAACT  | GCTGAATTT  | 120 |
| TAGCTGTTT  | GAGTTGATTG | GCACCACTGC | ACCACAACTC | AATATGAAAA  | CTATTTNACT | 180 |
| TATTATTAT  | CTTGTGAAAA | GTATACAATG | AAAATTTGT  | TCATACTGTA  | TTTATCAAGT | 240 |
| ATGATGAAAA | GCAATAGATA | TATATTCTTT | TATTATGTTN | AATTATGATT  | GCCATTATTA | 300 |
| ATCGGAAAAA | TGTGGAGTGT | ATGTTCTTT  | CACAGTAATA | TATGCCTTTT  | GTAACCTCAC | 360 |
| TTGGTTATT  | TATTGAAAT  | GAATTACAA  | ATTCTTAATT | TAAGAAAATG  | GTANGTTATA | 420 |
| TTTANTTCAN | TAATTCTTT  | CCITGTTAC  | GTAAATTG   | AAAAGAATGC  | AT         | 472 |

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| CTGAAGCATT  | TCTTCAAAC  | TNTCTACTTT | TGTCATTGAT | ACCTGTAGTA  | AGTTGACAAT | 60  |
| GTGGTGAAT   | TTCAAAATTA | TATGTAAC   | CTACTAGTTT | TACTTTCTCC  | CCCAAGTCTT | 120 |
| TTTTAACTCA  | TGATTTTAC  | ACACACAATC | CAGAACTTAT | TATATAGCCT  | CTAAGTCTTT | 180 |
| ATTCTTCACA  | GTAGATGATG | AAAGAGTCCT | CCAGTGTCTT | GNGCANAATG  | TTCTAGNTAT | 240 |
| AGCTGGATAC  | ATACNGTGGG | AGTTCTATAA | ACTCATACCT | CAGTGGGACT  | NAACCAAAAT | 300 |
| TGTGTTAGTC  | TCAATTCTCA | CCACACTGAG | GGAGCCTCCC | AAATCACTAT  | ATTCTTATCT | 360 |
| GCAGGTACTC  | CTCCAGAAA  | ACNGACAGGG | CAGGCTTGCA | TGAAAAAAGTN | ACATCTCGGT | 420 |
| TACAAAAGTCT | ATCTTCCTCA | NANGTCTGTN | AAGGAACAAT | TTAATCTTCT  | AGCTTT     | 476 |

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACTCTTCTA ATGCTGATAT GATCTTGAGT ATAAGAATGC ATATGTCACT AGAATGGATA

60

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAATAATGCT GCAAACCTAA TGTTCTTATG CAAAATGGAA CGCTAATGAA ACACAGCTTA | 120 |
| CAATCGCAA TCAAAACTCA CAAGTGCTCA TCTGTTGTAG ATTTAGTGTA ATAAGACTTA  | 180 |
| GATTGTGCTC CTTCGGATAT GATTGTTCT CANATCTGG GCAATNTTC TTAGTCAAAT    | 240 |
| CAGGCTACTA GAATTCTGTT ATTGGATATN TGAGAGCATG AAATTTTAA NAATACACTT  | 300 |
| GTGATTATNA AATTAATCAC AAATTCACT TATAACCTGCT ATCAGCAGCT AGAAAAACAT | 360 |
| NTNNNTTTTA NATCAAAGTA TTTTGTGTTT GGAANTGTNN AAATGAAATC TGAATGTGGG | 420 |
| TTCNATCTTA TTTTTCCCN GACNACTANT TNCTTTTTA GGGNCTATTC TGANCCATC    | 479 |

## (2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 461 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| AGTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTGT GGCACTGACA ATCAGACCTA   | 60  |
| TGCTAGTTCC TGTCACTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA   | 120 |
| TCAACTCCAG CTGGATTATT TTGGAGCTG CAAATCTATT CCTACTTGTA CGGACTTTGA   | 180 |
| AGTGATTCAG TTTCTCTAC GGATGAGAGA CTGACTCAAG AATATCCTCA TGCAGCTTTA   | 240 |
| TGAAGCCACT CTGAACACGC TGGTTATCTA GATGAGAACAA GAGAAATAAA GTCAGAAAAT | 300 |
| TTACCTGGAG AAAAGAGGCT TTGGCTGGGG ACCATCCCCT TGAACCTTCT CTTAAGGACT  | 360 |
| TTAAGAAAAA CTACCACATG TTGTGTATCC TGGTGCCTGGC CGTTTATGAA CTGACCACCC | 420 |
| TTTGAATAA TCTTGACGCT CCTGAACCTTG CCTCCTCTGCG A                     | 461 |

## (2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 171 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GTGGCCGCGC GCAGGTGTTT CCTCGTACCG CAGGGCCCCC TCCCTTCCCC AGGCGTCCCT | 60  |
| CGGCGCCTCT GCGGGCCCCA GGAGGAGCGG CTGGCGGGTG GGGGGAGTGT GACCCACCC  | 120 |
| CGGTGAGAAA AGCCTTCTCT AGCGATCTGA GAGGCGTGCC TTGGGGGTAC C          | 171 |

## (2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 269 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CGGCCGCAAG | TGCAACTCCA | GCTGGGGCCG | TGCGGACGAA | GATTCTGCCA | GCAGTTGGTC | 60  |
| CGACTGCGAC | GACGGCGGCC | GCGACAGTCG | CAGGTGCAGC | GCGGGCGCCT | GGGGTCTTGC | 120 |
| AAGGCTGAGC | TGACGCCGCA | GAGGCTGTGT | CACGTCCCAC | GACCTTGACG | CCGTCGGGGA | 180 |
| CAGCCGGAAC | AGAGCCCGGT | GAAGCGGGAG | GCCTCGGGGA | GCCCCTCGGG | AAGGGCGGCC | 240 |
| CGAGAGATAC | GCAGGTGCAG | GTGGCCGCC  |            |            |            | 269 |

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTGGAACATC | TACTGCGAGC | ACAGCAGGTC | AGCAACAAGT | TTATTTGCA  | 60  |
| GCTAGCAAGG | TAACAGGGTA  | GGGCATGGTT | ACATGTTCA  | GTCAACTTCC | TTTGTCTG   | 120 |
| TTGATTGGTT | TGTCTTTATG  | GGGGCGGGGT | GGGGTAGGGG | AAACGAAGCA | AATAACATGG | 180 |
| AGTGGGTGCA | CCCTCCCTGT  | AGAACCTGGT | TACAAAGCTT | GGGGCAGTTC | ACCTGGTCTG | 240 |
| TGACCGTCAT | TTCTTGACA   | TCAATGTTAT | TAGAAGTCAG | GATATCTTTT | AGAGAGTCCA | 300 |
| CTGTTCTGGA | GGGAGATTAG  | GGTTTCTTGC | CAAATCCAAC | AAAATCCACT | AAAAAAGTTG | 360 |
| GATGATCAGT | ACGAATACCG  | AGGCATATTC | TCATATCGGT | GGCCA      |            | 405 |

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTTTTT  | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | 60  |
| GGCACTTAAT | CCATTTTTAT  | TTCAAAATGT | CTACAAATTT | AATCCCATTA | TACGGTATTT | 120 |
| TCAAAATCTA | AATTATTCAA  | ATTAGCCAAA | TCCTTACCAA | ATAATACCA  | AAAATCAAAA | 180 |
| ATATATCTCT | TTCAGCAAAC  | TTGTTACATA | AATTAACAAA | ATATATACGG | CTGGTGT    | 240 |
| CAAAGTACAA | TTATCTTAAAC | ACTGCAAACA | TTTTAAGGAA | CTAAAATAAA | AAAAAACACT | 300 |
| CCGCAAAGGT | TAAAGGGAAC  | AACAAATTCT | TTTACAACAC | CATTATAAAA | ATCATATCTC | 360 |
| AAATCTTAGG | GAATATATA   | CTTCACACGG | GATCTTAAC  | TTTACTCACT | TTGTTATTT  | 420 |
| TTTAAACCA  | TTGTTGGGC   | CCAACACAAT | GGAATCCCCC | CTGGACTAGT |            | 470 |

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 581 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

|                       |            |            |            |            |     |
|-----------------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT TTTTTTTTGA | CCCCCCTCTT | ATAAAAACA  | AGTTACCATT | TTATTTACT  | 60  |
| TACACATATT            | TATTTTATAA | TTGGTATTAG | ATATCAAA   | GGCACCTTT  | 120 |
| TAAATGGAAA            | CTGCCCTAGA | TACATAATT  | TTAGGAATT  | GCTAAAATC  | 180 |
| GAAAATCTTC            | TCTAGCTCTT | TTGACTGTAA | ATTTTGACT  | CTTGTAAAAC | 240 |
| ATTTTCTTG             | TCTTTAAAT  | TATCTAAC   | TTCCATT    | ATCCAAATTC | 300 |
| GCTTCTCTAG            | CCTCATTTCC | TAGCTCTTAT | CTACTATTAG | AAAGTCAATT | 360 |
| AGGGAAAACA            | GGAAGAGAAA | TGGCACACAA | AACAAACATT | TTAGTGGCTT | 420 |
| ACGTTAATAA            | AATAGCATT  | TGTGAAGCCA | GCTAAAAGA  | AGGCTTAGAT | 480 |
| CCATTTAGT             | CACTAACAGA | TATCAAAGTG | CCAGAATGCA | AAAGGTTGT  | 540 |
| TCAAAAGCTA            | ATATAAGATA | TTTCACATAC | TCATCTTCT  | G          | 581 |

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 578 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

|                       |            |            |             |     |
|-----------------------|------------|------------|-------------|-----|
| TTTTTTTTTT TTTTTCTCTT | CTTTTTTTTT | GAAATGAGGA | TCGAGTTTT   | 60  |
| CACTCTCTAG            | ATAGGGCATG | AAGAAAATC  | ATCTTCCAG   | 120 |
| CTCTTATGCT            | ATATCATATT | TTAAGTTAAA | CTAATGAGTC  | 180 |
| AGGAAATCTG            | TTCATTCTTC | TCATTATAT  | AGTTATATCA  | 240 |
| GAGGTTTTTC            | TTCTCTATT  | ACACATAT   | TTCCATGTGA  | 300 |
| TTCATGCAAA            | CTAGAAAATA | ATGTTCTTT  | TGCATAAGAG  | 360 |
| CAAAACTGCT            | CAAATTGTTT | GTAAAGTTAT | AAAGAGAACAA | 420 |
| AAATCACATT            | TACGACAGCA | ATAATAAAC  | TGAAGTACCA  | 480 |
| AAAGGAACAT            | TTTTAGCCTG | GTATAATTA  | GTAAATATC   | 540 |
| TGAATTCA              | TGTTATTATT | GCTAATT    | TTTACAAGCA  | 578 |
|                       |            | CACAATGG   |             |     |

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 538 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTTTTTTTTT TTTTCAGTA ATAATCAGAA CAATATTTAT TTTTATATTAA AAAATTCTATA | 60  |
| GAAAAGTGC TTACATTTAA TAAAAGTTG TTTCTCAAAG TGATCAGAGG AATTAGATAT    | 120 |
| GTCTTGAAACA CCAATATTAA TTTGAGGAAA ATACACCAAA ATACATTAAG TAAATTATTT | 180 |
| AAGATCATAG AGCTTGAAAG TGAAAAGATA AAATTGACCC TGAGAAACTC TGAGCATTTA  | 240 |
| AAATCCACTA TTAGCAAATA ATTACTATG GACTCTTGC TTTAATTTTG TGATGAATAT    | 300 |
| GGGGTGTAC TGGTAAACCA ACACATTCTG AAGGATACAT TACTTAGTGA TAGATTCTTA   | 360 |
| TGTACTTTGC TAATACGTGG ATATGAGTTG ACAAGTTCT CTTCTTCAA TCTTTAAGG     | 420 |
| GGCGAGAAAT GAGGAAGAAA AGAAAAGGAT TACGCCACT GTTCTTCTA TGGAAGGATT    | 480 |
| AGATATGTTT CCTTTGCCAA TATTAAGAAA ATAATAATGT TTACTACTAG TGAAACCC    | 538 |

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| TTTTTTTTTT TTTTTAGTC AAGTTCTAT TTTTATTATA ATTAAAGTCT TGGTCATTTC     | 60  |
| ATTATTTAGC TCTGCAACTT ACATATTTAA ATTAAAGAAA CGTTTTAGAC AACTGTACAA   | 120 |
| TTTATAAAATG TAAGGTGCCA TTATTGAGTA ATATATTCCCT CCAAGAGTGG ATGTGTCCCT | 180 |
| TCTCCCCACCA ACTAATGAAC AGCAACATTA GTTTAATTTT ATTAGTAGAT ATACACTGCT  | 240 |
| GCAAACGCTA ATTCTCTTCT CCATCCCCAT GTGATATTGT GTATATGTGT GAGTTGGTAG   | 300 |
| AATGCATCAC AATCTACAAAT CAACAGCAAG ATGAAGCTAG GCTGGGCTTT CGGTGAAAAT  | 360 |
| AGACTGTGTC TGTCTGAATC AAATGATCTG ACCTATCCTC GGTGGCAAGA ACTCTTCGAA   | 420 |
| CCGCTTCCTC AAAGGCCTG CCACATTGT GGCTCTTGC ACTTGTTCGA AAA             | 473 |

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| CGCCATGGCA CTGCAGGGCA TCTCGGTCTAT GGAGCTGTCC GGCCTGGCCC CGGGCCCGTT | 60  |
| CTGTGCTATG GTCTCTGGCTG ACTTCGGGGC GCGTGTGGTA CGCGTGGACC GGCCCGGCTC | 120 |
| CCGCTACGAC GTGAGCCGCT TGGGCCGGGG CAAGCGCTCG CTAGTGCTGG ACCTGAAGCA  | 180 |
| GCCCGGGGGA GCCGCCGTGC TGCGGGCTCT GTGCAAGCGG TCGGATGTGC TGCTGGAGCC  | 240 |
| CTTCCGCGCGC GGTGTCTATGG AGAAACTCCA GCTGGGCCA GAGATTCTGC AGCGGGAAAA | 300 |
| TCCAAGGCTT ATTTATGCCA GGCTGAGTGG ATTTGGCCAG TCAGGAAGCT TCTGCGGTT   | 360 |
| AGCTGGCCAC GATATCAACT ATTTGGCTTT GTCAAGGTGTT CTCTCAAAAA TTGGCAGAAG | 420 |
| TGGTGAGAAT CCGTATGCC CGCTGAATCT CCTGGCTGAC TTGCTGGTG GTGGCCTTAT    | 480 |
| GTGTGCACTG GGCATTATAA TGGCTCTTT TGACCGCACA CGCACTGACA AGGGTCAGGT   | 540 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| CATTGATGCA AATATGGTGG AAGGAACAGC ATATTAAGT TCTTTCTGT GGAAAACCTCA   | 600  |
| GAAATCGAGT CTGTGGAAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTTT  | 660  |
| CTATACGACT TACAGGACAG CAGATGGGA ATTCACTGGCT GTTGGAGCAA TAGAACCCCA  | 720  |
| GTTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAACTTC CCAATCAGAT  | 780  |
| GAGCATGGAT GATTGGCCAG AAATGAAGAA GAAGTTTGCA GATGTATTTG CAAAGAAGAC  | 840  |
| GAAGGCAGAG TGGTGTCAAA TCTTGACGG CACAGATGCC TGTTGACTC CGGTTCTGAC    | 900  |
| TTTTGAGGAG GTTGTTCATC ATGATCACAA CAAGGAAACGG GGCTCGTTA TCACCAGTGA  | 960  |
| GGAGCAGGAC GTGAGCCCCC GCCCTGCACC TCTGCTGTTA AACACCCCA CCATCCCTTC   | 1020 |
| TTTCAAAAGG GATCCTTCA TAGGAGAACAA CACTGAGGAG ATACTTGAAG AATTGGATT   | 1080 |
| CAGCCCGAA GAGATTTATC AGCTTAACTC AGATAAAATC ATTGAAAGTA ATAAGGTA     | 1140 |
| AGCTAGTCTC TAACCTCCAG GCCCACGGCT CAAGTGAATT TGAATACTGC ATTTACAGTG  | 1200 |
| TAGAGTAACA CATAACATTG TATGCATGGA AACATGGAGG AACAGTATTAA CAGTGTCTTA | 1260 |
| CCACTCTAAT CAAGAAAAGA ATTACAGACT CTGATTCTAC AGTGATGATT GAATTCTAAA  | 1320 |
| AATGGTTATC ATTAGGGCTT TTGATTATA AAACTTGGG TACTTATACT AAATTATGGT    | 1380 |
| AGTTATTCTG CCTTCCAGTT TGCTTGATAT ATTTGTTGAT ATTAAGATTG TTGACTTATA  | 1440 |
| TTTTGAATGG GTTCTAGTGA AAAAGGAATG ATATATTCTT GAAGACATCG ATATACATT   | 1500 |
| ATTTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAAT GCCACAAATT GTATGGTGAT  | 1560 |
| AAAAGTCACG TGAACACAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 1620 |
| A                                                                  | 1621 |

## (2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro |  |
| 1 5 10 15                                                       |  |
| Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val |  |
| 20 25 30                                                        |  |
| Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg |  |
| 35 40 45                                                        |  |
| Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala |  |
| 50 55 60                                                        |  |
| Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe |  |
| 65 70 75 80                                                     |  |
| Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln |  |
| 85 90 95                                                        |  |
| Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln |  |
| 100 105 110                                                     |  |
| Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala |  |
| 115 120 125                                                     |  |
| Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr |  |
| 130 135 140                                                     |  |
| Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Leu Met Cys     |  |
| 145 150 155 160                                                 |  |
| Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys |  |
| 165 170 175                                                     |  |
| Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser |  |
| 180 185 190                                                     |  |
| Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg |  |
| 195 200 205                                                     |  |

Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg  
 210                    215                    220  
 Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe  
 225                    230                    235                    240  
 Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro  
 245                    250                    255  
 Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala  
 260                    265                    270  
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp  
 275                    280                    285  
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val  
 290                    295                    300  
 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu  
 305                    310                    315                    320  
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala  
 325                    330                    335  
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu  
 340                    345                    350  
 Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn  
 355                    360                    365  
 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu  
 370                    375                    380

## (2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1524 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

|             |             |             |            |            |            |      |
|-------------|-------------|-------------|------------|------------|------------|------|
| GGCACGAGCC  | TGCGCCAGGG  | CCTGAGCGGA  | GGCGGGGGCA | GCCTCGCCAG | CGGGGGCCCC | 60   |
| GGGCCCTGGCC | ATGCCTCACT  | GAGCCAGCGC  | CTGGCCCTCT | ACCTCGCCGA | CAGCTGGAAC | 120  |
| CAGTGCAGCC  | TAGTGGCTCT  | CACCTGCTTC  | CTCCTGGCG  | TGGGCTGCCG | GCTGACCCCG | 180  |
| GGTTTTGTACC | ACCTGGGGCG  | CACTGCTTC   | TGCATCGACT | TCATGGTTTT | CACGGTGCAG | 240  |
| CTGCTTACA   | TCTTCACGGT  | CAACAAACAG  | CTGGGGCCCA | AGATCGTCAT | CGTGAGCAAG | 300  |
| ATGATGAAGG  | ACGTGTTCTT  | CTTCCTCTC   | TTCCCTGGCG | TGTGGCTGGT | AGCCTATGGC | 360  |
| GTGGCCACGG  | AGGGGCTCTT  | GAGGCCACGG  | GACAGTGA   | TCCCAAGTAT | CCTGCGCCGC | 420  |
| GTCTTCTACC  | GTCCCTACCT  | GCAGATCTTC  | GGGCAGATTG | CCCAGGAGGA | CATGGACGTG | 480  |
| GCCCTCATGG  | AGCACAGCAA  | CTGCTCGTCG  | GAGCCGGCT  | TCTGGGCACA | CCCTCCTGGG | 540  |
| GCCCAGGCGG  | GCACCTGCGT  | CTCCCAAGTAT | GCCAACCTGC | TGGTGGTGCT | GCTCCTCGTC | 600  |
| ATCTTCTTCG  | TCTGCCCCAA  | CATCCCTGCTG | GTCAACTTGC | TCATTGCCAT | GTTCAGTIA  | 660  |
| ACATTCGGCA  | AACTACAGGG  | CAACAGCGAT  | CTCTACTGGA | AGGCGCAGCG | TTACCGCCTC | 720  |
| ATCCGGGAAT  | TCCACTCTCG  | GCCCCGCGCTG | GCCCCGCCCT | TTATCGTCAT | CTCCCACTTG | 780  |
| CGCCTCTTCG  | TCAGGCAATT  | GTGCAGGGGA  | CCCCGGAGCC | CCCAGCCGTC | CTCCCCGGCC | 840  |
| CTCGAGCATT  | TCCGGGTTTA  | CCTTTCTAAG  | GAAGCCGAGC | GGAGCTGCT  | AACGTGGAA  | 900  |
| TCGGTGCATA  | AGGAGAACCTT | TCTGCTGGCA  | CGCGCTAGGG | ACAAGCGGGA | GAGCGACTCC | 960  |
| GAGCGTCTGA  | AGCGCACGTC  | CCAGAAGGTG  | GACTTGGCAC | TGAAACAGCT | GGGACACATC | 1020 |
| CGCGAGTACG  | AACAGCGCCT  | GAAAGTGTG   | GAGCGGGAGG | TCCAGCAGTG | TAGCCCGCTC | 1080 |
| CTGGGGTGGG  | TGGCCGAGGC  | CCTGAGCCGC  | TCTGCCCTGC | TGCCCGCAGG | TGGGCCGCCA | 1140 |
| CCCCCTGACC  | TGCCCTGGGTC | CAAAGACTGA  | GCCCTGCTGG | CGGACTTCAA | GGAGAAGGCC | 1200 |
| CCACAGGGGA  | TTTGCTCCT   | AGAGTAAGGC  | TCATCTGGGC | CTCGGCCCCC | GCACCTGGTG | 1260 |
| GCCTTGTCT   | TGAGGTGAGC  | CCCATGTCCA  | TCTGGGCCAC | TGTCAGGACC | ACCTTTGGGA | 1320 |
| GTGTCATCCT  | TACAAACCAC  | AGCATGCCG   | GCTCCTCCCA | GAACCAGTCC | CAGCCTGGGA | 1380 |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| GGATCAAGGC CTGGATCCCC GGCGTATTC CATCTGGAGG CTGCAGGGTC CTTGGGTAA | 1440 |
| CAGGGACAC AGACCCCTCA CCACTCACAG ATTCTCACA CTGGGAAAT AAAGCCATT   | 1500 |
| CAGAGGAAAA AAAAAAAAAA AAAA                                      | 1524 |

## (2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GGGAACCAGC CTGCACGCGC TGGCTCCGGG TGACAGCCGC GCGCCTCGGC CAGGATCTGA  | 60   |
| GTGATGAGAC GTGTCCCCAC TGAGGTGCC CACAGCAGCA GGTGTTGAGC ATGGGCTGAG   | 120  |
| AAGCTGGACC GGCACCAAAG GGCTGGCAGA AATGGGCGCC TGGCTGATTC CTAGGCAGTT  | 180  |
| GGCGGCAGCA AGGAGGAGAG GCCGCAGCTT CTGGAGCAGA GCGGAGACGA AGCAGTTCTG  | 240  |
| GAGTGCCTGA ACGGCCCTACG GAGCCCTACC CGCCTGGCCC ACTATGGTCC AGAGGCTGTG | 300  |
| GGTGAGCCGC CTGCTGCAGGC ACCGGAAAGC CCAGCTCTTG CTGCTCAACC TGCTAACCTT | 360  |
| TGGCCTGGAG GTGTGTTGG CGCGAGCAT CACCTATGTG CCGCCTCTGC TGCTGGAAGT    | 420  |
| GGGGTAGAG GAGAAGTTCA TGACCATGGT GCTGGCATT GGTCAGTGC TGGGCTGGT      | 480  |
| CTGTGTCCTG CTCCCTAGGCT CAGCCAGTGA CCACTGGCGT GGACGCTATG GCCGCCCG   | 540  |
| GCCCTTCATC TGGCACTGT CCTTGGCAT CCTGCTGAGC CTCTTCTCA TCCAAGGGC      | 600  |
| CGGCTGGCTA GCAGGGCTGC TGTGCCCGGA TCCCAGGCC CTGGAGCTGG CACTGCTCAT   | 660  |
| CCTGGGCGTG GGGCTGCTGG ACTTCTGTGG CCAGGTGTGC TTCACTCCAC TGGAGGCCCT  | 720  |
| GCTCTCTGAC CTCTTCCGGG ACCCGGACCA CTGTCGCCAG GCCTACTCTG TCTATGCCTT  | 780  |
| CATGATCAGT CTTGGGGGCT GCCTGGGCTA CCTCCTGCTC GCCATTGACT GGGACACAG   | 840  |
| TGCCCTGGCC CCCTACCTGG GCACCCAGGA GGAGTGCCTC TTTGGCCTGC TCACCCCTCAT | 900  |
| CTTCCTCACC TGGTAGCAG CCACACTGCT GGTGGCTGAG GAGGCAGCGC TGGGGCCAC    | 960  |
| CGAGCCAGCA GAAGGGCTGT CGGCCCTCTC CTTGTCGCC CACTGCTGTC CATGCCGGC    | 1020 |
| CCGCTTGGCT TTCCGGAACCC TGGGCGCCCT GCTTCCCCGG CTGACCGACG TGTGCTGCCG | 1080 |
| CATGCCCGC ACCCTGCGCC GGCTCTTCGT GGCTGAGCTG TGCACTGGA TGGCACTCAT    | 1140 |
| GACCTTCACG CTGTTTACA CGGATTTCTGT GGGCGAGGGG CTGTACCAAGG CGCTGCCAG  | 1200 |
| AGCTGAGCCG GGCACCGAGG CCCGGAGACA CTATGATGAA GGCGTTCGGA TGGGAGCCT   | 1260 |
| GGGGCTGTTG CTGCAGTGC CGCATCTCCCT GGTCTCTCT CTGGTCATGG ACCGGCTGGT   | 1320 |
| GCAGCGATTG GGCACTCGAG CAGTCATTTT GGCCAGTGTG GCAGCTTCTC CTGCTGCC    | 1380 |
| CGGTGCCACA TGCTGTCCC ACAGTGTGGC CGTGGTACCA GCTTCAGCCG CCCTCACCGG   | 1440 |
| GTTCACCTTC TCAGCCCTGC AGATCCTGCC CTACACACTG GCCTCCCTCT ACCACCGGA   | 1500 |
| GAAGCAGGTG TTCCCTGCCA AATACCGAGG GGACACTGGA GGTGCTAGCA GTGAGGACAG  | 1560 |
| CCTGATGACC AGCTTCTGC CAGGCCCTAA GCCTGGAGCT CCCTTCCCTA ATGGACACGT   | 1620 |
| GGGTGCTGGA GGCAGTGGCC TGCTCCACCC TCCACCGCG CTCTGCGGGG CCTCTGCC     | 1680 |
| TGATGTCCTCC GTACGTGTGG TGGTGGGTGA GCCCACCGAG GCCAGGGTGG TTCCGGGCC  | 1740 |
| GGGCATCTGC CTGGACCTCG CCATCCTGGA TAGTGCCTC CTGCTGTCCTC AGGTGGCCC   | 1800 |
| ATCCCTGTTT ATGGGCTCCA TTGTCCAGCT CAGCCAGTCT GTCACGCTCT ATATGGTGT   | 1860 |
| TGCCGCAGGC CTGGTCTGG TCGCCATTAA CTTTGCTACA CAGGTAGTAT TTGACAAGAG   | 1920 |
| CGACTTGGCC AAATACTCAG CGTAGAAAAC TTCCACGACA TTGGGGTGGA GGGCCTGCC   | 1980 |
| CACTGGGTCC CAGCTCCCCG CTCCCTGTTAG CCCCATGGG CTGCCGGGCT GGCCGCCAGT  | 2040 |
| TTCTGTTGCT GCCAAAGTAA TGTGGCTCTC TGCTGCCACC CTGCTGCTGCT GAGGTGCC   | 2100 |
| GCTGCACAGC TGGGGGCTGG GGCGTCCCTC TCCCTCTCC CCAGTCTCTA GGGCTGCC     | 2160 |
| ACTGGAGGCC TTCCAAGGGG GTTTCAGTCT GGACTTATAC AGGGAGGCCA GAAGGGCTCC  | 2220 |
| ATGCACTGGA ATGCCGGGAC TCTGCAGGTG CATTACCCAG GCTCAGGGTT AACAGCTAGC  | 2280 |
| CTCCTAGTTG AGACACACCT AGAGAAGGGT TTTTGGGAGC TGAATAAACT CAGTCACCTG  | 2340 |
| GTTCCTCCATC TCTAAGCCCC TTAACCTGCA GCTTCGTTA ATGTAGCTCT TGCACTGGAG  | 2400 |
| TTTCTAGGAT GAAACACTCC TCCATGGGAT TTGAACATAT GACTTATTG TAGGGGAAGA   | 2460 |
| GTCCTGAGGG GCAACACACA AGAACCAAGGT CCCCTCAGCC CACAGCACTG TCTTTTGCT  | 2520 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GATCCACCCC CCTCTTACCT TTTATCAGGA TGTGGCCTGT TGGTCCTTCT GTGCCATCA   | 2580 |
| CAGAGACACA GGCATTTAAA TATTTAACCT ATTTATTTAA CAAAGTAGAA GGGATCCAT   | 2640 |
| TGCTAGCTTT TCTGTGTTGG TGTCTAATAT TTGGGTAGGG TGCGGATCC CCAACAATCA   | 2700 |
| GGTCCCTGA GATAGCTGGT CATTGGCTG ATCATTGCCA GAATCTTCTT CTCCCTGGGT    | 2760 |
| CTGGCCCCCC AAAATGCCA ACCCAGGACC TTGGAAATTCT TACTCATCCC AAATGATAAT  | 2820 |
| TCCAAATGCT GTTACCCAAG GTTGGGTGT TGAAGGAAGG TAGAGGGTGG GGCTTCAGGT   | 2880 |
| CTCAACGGCT TCCCTAACCA CCCCTCTTCT CTTGGCCAG CCTGGTTCCTC CCCACTTCCA  | 2940 |
| CTCCCCCTCA CTCTCTCTAG GACTGGCTG ATGAAGGCAC TGCCCAAAT TTCCCCCTACC   | 3000 |
| CCCAACTTC CCCTACCCCCC AACTTCCCC ACCAGCTCCA CAACCCCTGTT TGGAGCTACT  | 3060 |
| GCAGGACCAAG AAGCACAAAG TGCGGTTCC CAAGCCTTTC TCCATCTCAG CCCCCAGAGT  | 3120 |
| ATATCTGTGC TTGGGAATC TCACACAGAA ACTCAGGAGC ACCCCCTGCC TGAGCTAAGG   | 3180 |
| GAGGTCTTAT CTCTCAGGGG GGGTTAAAGT GCCGTTTGCA ATAATGTCGT CTTATTATT   | 3240 |
| TAGCAGGGGTG AATATTTTAT ACTGTAAGTG AGCAATCAGA GTATAATGTT TATGGTGACA | 3300 |
| AAATTAAGG CTTCTTATA TGTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA    | 3360 |
| AAAAAAAAARA AAAAAAAAAA AAAAAAAAAA AAAAAAATAA AAAAAAAAAA            | 3410 |

## (2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| AGCCAGGCGT CCCTCTGCCT GCCCCACTCAG TGGCAACACC CGGGAGCTGT TTTGTCCTT  | 60   |
| GTGGAGCCTC AGCAGTTCCC TCTTTCAGAA CTCACTGCCA AGAGCCTGA ACAGGAGCCA   | 120  |
| CCATGCAGTG CTTCAGCTTC ATTAAGACCA TGATGATCCT CTTCAATTG CTCATCTTC    | 180  |
| TGTGTGGTGC AGCCCTGTTG GCAGTGGCA TCTGGGTGTC AACATGATGGG GCATCCTTC   | 240  |
| TGAAGATCTT CGGGCCACTG TCGTCCAGTG CCATGCAGTT TGTCACGTG GGCTACTTCC   | 300  |
| TCATCGCAGC CGGCCTTGTG GTCTTTGTC TTGGTTTCTC GGGCTGCTAT GGTGCTAAGA   | 360  |
| CTGAGAGCAA GTGTGCCCTC GTGACGTTCT TCTTCATCCT CCTCCATC TTCATTGCTG    | 420  |
| AGGTTGCAGC TGCTGTGGTC GCCTTGGTGT ACACCACAAT GGCTGAGCAC TTCCTGACGT  | 480  |
| TGCTGGTAGT GCCTGCCATC AAGAAAGATT ATGGTCCCA GGAAGACTTC ACTCAAGTGT   | 540  |
| GGAACACCCAC CATGAAAGGG CTCAAAGTGT GTGGCTTCAC CAACTATACG GATTTTGAGG | 600  |
| ACTCACCCATA CTTCAAAGAG AACAGTCCCT TTCCCCCATT CTGTTGCAAT GACAACGTCA | 660  |
| CCAACACAGC CAATGAAACC TGCACCAAGC AAAAGGCTCA CGACCAAAAA GTAGAGGGTT  | 720  |
| GCTTCATCA GCTTTGTAT GACATCCGAA CTAATCGAGT CACCGTGGGT GGTGTGGCAG    | 780  |
| CTGGAATTGG GGCCCTCGAG CTGGCTGCCA TGATTGTGTC CATGTATCTG TACTGCAATC  | 840  |
| TACAATAAGT CCACTTCTGC CTCTGCCACT ACTGCTGCCA CATGGGAACG GTGAAGAGGC  | 900  |
| ACCCCTGGCAA GCAGCAGTGA TTGGGGGAGG GGACAGGATC TAACAATGTC ACTTGGGCCA | 960  |
| GAATGGACCT GCCCTTTCTG CTCCAGACTT GGGGCTAGAT AGGGACCACT CCTTTTACCG  | 1020 |
| ATGCTGACT TTCCCTTCCAT TGGTGGTGG ATGGGTGGGG GGCATTCAG AGCCTCTAAG    | 1080 |
| GTAGCCAGTT CTGTTGCCA TTCCCCCAGT CTATTAACCC CTTGATATGC CCCCTAGGCC   | 1140 |
| TAGTGGTGT CCCAGTGTCTC TACTGGGGA TGAGAGAAAG GCATTTATA GCCTGGCAT     | 1200 |
| AAGTGAAATC AGCAGAGCCT CTGGGTGGAT GTGTAGAAGG CACTTCAAAA TGCATAAACCC | 1260 |
| TGTTACAATG TTAAAAAAA AAAAAAAAAA                                    | 1289 |

## (2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln  
1 5 10 15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe  
20 25 30

Phe Phe Leu Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala  
35 40 45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu  
50 55 60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro  
65 70 75 80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser  
85 90 95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys  
100 105 110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Val Ile Phe  
115 120 125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe  
130 135 140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys  
145 150 155 160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu  
165 170 175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Arg Gln  
180 185 190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu  
195 200 205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr  
210 215 220

Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp  
225 230 235 240

Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val  
245 250 255

Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg  
260 265 270

Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly  
275 280 285

Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly  
 290                    295                    300

Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp  
 305                    310                    315

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 553 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala  
 1                    5                    10                    15

Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu  
 20                    25                    30

Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val  
 35                    40                    45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
 50                    55                    60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly  
 65                    70                    75                    80

Arg Tyr Gly Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile  
 85                    90                    95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
 100                    105                    110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly  
 115                    120                    125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
 130                    135                    140

Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
 145                    150                    155                    160

Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
 165                    170                    175

Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
 180                    185                    190

Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
 195                    200                    205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly  
 210 215 220  
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His  
 225 230 235 240  
 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu  
 245 250 255  
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg  
 260 265 270  
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
 275 280 285  
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
 290 295 300  
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
 305 310 315 320  
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
 325 330 335  
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
 340 345 350  
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
 355 360 365  
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
 370 375 380  
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
 385 390 395 400  
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
 405 410 415  
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
 420 425 430  
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
 435 440 445  
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser  
 450 455 460  
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
 465 470 475 480  
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
 485 490 495  
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
 500 505 510  
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
 515 520 525  
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp

|     |     |     |
|-----|-----|-----|
| 530 | 535 | 540 |
|-----|-----|-----|

|                                     |     |     |
|-------------------------------------|-----|-----|
| Lys Ser Asp Leu Ala Lys Tyr Ser Ala | 545 | 550 |
|-------------------------------------|-----|-----|

## (2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

|                                                                 |   |   |
|-----------------------------------------------------------------|---|---|
| Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu | 1 | 5 |
|-----------------------------------------------------------------|---|---|

|    |  |    |
|----|--|----|
| 10 |  | 15 |
|----|--|----|

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val | 20 | 25 |
|-----------------------------------------------------------------|----|----|

|    |  |  |
|----|--|--|
| 30 |  |  |
|----|--|--|

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser | 35 | 40 |
|-----------------------------------------------------------------|----|----|

|    |  |  |
|----|--|--|
| 45 |  |  |
|----|--|--|

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly | 50 | 55 |
|-----------------------------------------------------------------|----|----|

|    |  |  |
|----|--|--|
| 60 |  |  |
|----|--|--|

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr | 65 | 70 |
|-----------------------------------------------------------------|----|----|

|    |  |    |
|----|--|----|
| 75 |  | 80 |
|----|--|----|

|                                                             |    |    |
|-------------------------------------------------------------|----|----|
| Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Ile | 85 | 90 |
|-------------------------------------------------------------|----|----|

|    |  |  |
|----|--|--|
| 95 |  |  |
|----|--|--|

|                                                             |     |     |
|-------------------------------------------------------------|-----|-----|
| Phe Ile Ala Glu Val Ala Ala Val Val Ala Leu Val Tyr Thr Thr | 100 | 105 |
|-------------------------------------------------------------|-----|-----|

|     |  |  |
|-----|--|--|
| 110 |  |  |
|-----|--|--|

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys | 115 | 120 |
|-----------------------------------------------------------------|-----|-----|

|     |  |  |
|-----|--|--|
| 125 |  |  |
|-----|--|--|

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met | 130 | 135 |
|-----------------------------------------------------------------|-----|-----|

|     |  |  |
|-----|--|--|
| 140 |  |  |
|-----|--|--|

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp | 145 | 150 |
|-----------------------------------------------------------------|-----|-----|

|     |  |     |
|-----|--|-----|
| 155 |  | 160 |
|-----|--|-----|

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn | 165 | 170 |
|-----------------------------------------------------------------|-----|-----|

|     |  |  |
|-----|--|--|
| 175 |  |  |
|-----|--|--|

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala | 180 | 185 |
|-----------------------------------------------------------------|-----|-----|

|     |  |  |
|-----|--|--|
| 190 |  |  |
|-----|--|--|

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile | 195 | 200 |
|-----------------------------------------------------------------|-----|-----|

|     |  |  |
|-----|--|--|
| 205 |  |  |
|-----|--|--|

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly | 210 | 215 |
|-----------------------------------------------------------------|-----|-----|

|     |  |  |
|-----|--|--|
| 220 |  |  |
|-----|--|--|

Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu  
 225                    230                    235                    240

Gln

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 366 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GCTCTTCCTC | TCCCTCCTC  | TGAATTTAAT | TCTTCAACT  | TGCAATTG   | AAGGATTACA | 60  |
| CATTTCACTG | TGATGTATAT | TGTGTTGCAA | AAAAAAA    | GTGCTTTGT  | TTAAAATTAC | 120 |
| TTGGTTTG   | AATCCATCTT | GCTTTTCCC  | CATTGGAACT | AGTCATTAAC | CCATCTCTGA | 180 |
| ACTGGTAGAA | AAACATCTGA | AGAGCTAGTC | TATCAGCATC | TGACAGGTGA | ATTGGATGGT | 240 |
| TCTCAGAAC  | ATTTCACCCA | GACAGCCTGT | TTCTATCCTG | TTAATAAAAT | TAGTTGGGT  | 300 |
| TCTCTACATG | CATAACAAAC | CCTGCTCAA  | TCTGTCACAT | AAAAGTCTGT | GACTTGAAGT | 360 |
| TTAGTC     |            |            |            |            |            | 366 |

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 282 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| ACAAAGATGA | ACCATTTCT  | ATATTATAGC | AAAATAAAAA  | TCTACCGTA  | TTCTAATATT | 60  |
| GAGAAATGAG | ATNAAACACA | ATNTTATAAA | GTCTACTTAG  | AGAAGATCAA | GTGACCTCAA | 120 |
| AGACTTTACT | ATTTCTATAT | TTAAGACAC  | ATGATTATC   | CTATTTAGT  | AACCTGGTTC | 180 |
| ATACGTTAAA | CAAAGGATAA | TGTGAACAGC | AGAGAGGATT  | TGTTGGCAGA | AAATCTATGT | 240 |
| TCAATCTNGA | ACTATCTANA | TCACAGACAT | TTCTATTCCCT | TT         |            | 282 |

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACACATGTCG CTTCACTGCC TTCTTAGATG CTTCTGGTCA ACATANAGGA ACAGGGACCA  | 60  |
| TATTTATCCT CCCTCCTGAA ACAATTGCAA AATAANACAA AATATATGAA ACAATTGCAA  | 120 |
| AATAAGGCAA AATATATGAA ACAACAGGTC TCGAGATATT GGAAATCAGT CAATGAAGGA  | 180 |
| TACTGATCCC TGATCACTGT CCTAATGCAG GATGTGGAA ACAGATGAGG TCACCTCTGT   | 240 |
| GACTGCCCCA GCTTAUTGCC TGTAGAGAGT TTCTANGCTG CAGTTCAAGAC AGGGAGAAAT | 300 |
| TGGGT                                                              | 305 |

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

|                                                                    |    |
|--------------------------------------------------------------------|----|
| ACCAAGGTGT NTGAATCTCT GACGTGGGAA TCTCTGATTG CCGCACAAATC TGAGTGGAAA | 60 |
| AANTCCTGGG T                                                       | 71 |

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCACA | 60  |
| GAAAATGGGG TGAAATTGGC CAACTTTCTA TNAACTTATG TTGGCAANTT TGCCACCAAC | 120 |
| AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCACTAANC GGAATTAANT | 180 |
| AATGGANTCA AGANACTCCC AGGCCTCAGC GT                               | 212 |

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

|                                                                   |    |
|-------------------------------------------------------------------|----|
| ACTCGTTGCA NATCAGGGGC CCCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC | 60 |
| CTCCGCCGGC GCAGAACATG CTGGGGTGGT                                  | 90 |

## (2) INFORMATION FOR SEQ ID NO:121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TGTANC GTGA ANACGACAGA NAGGGTTGTC AAAATGGAG AANCCTTGAA GTCATTTGAA  | 60  |
| GAATAAGATT TGCTAAAAGA TTTGGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG  | 120 |
| ATATNCANGT AAATTANGGA ATGAATTCTAT GGTTCTTTG GGAATTCCCTT TACGATNGCC | 180 |
| AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA                          | 218 |

## (2) INFORMATION FOR SEQ ID NO:122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG | 60  |
| CATTTGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT | 120 |
| CACCACCCCG GCGGGGTCAT CTGTGCCACA GGTCCCTGTT GACAGTGCAG            | 171 |

## (2) INFORMATION FOR SEQ ID NO:123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

|                                                                   |    |
|-------------------------------------------------------------------|----|
| TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA | 60 |
| TTATCAANTA TTGTGT                                                 | 76 |

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACCTTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT  | 60  |
| CAATGTGCTG GGTCAATATGG AGGGGAGGAG ACTCTAAAAT AGCCAATTTT ATTCTCTTGG | 120 |
| TTAAGAGTTTG T                                                      | 131 |

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTC GTTACCAACT ATACCACTGG   | 60  |
| CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGACT TTTGCTCAGA TGCTGAAGAA    | 120 |
| CTACAGCTG CATTGGCAG AAATGAAGAT GAATTTGGAT TAAATGAGGA TGCTGAAGAT    | 180 |
| TTGCCTCACCC AAACAAAAGT GAAACAACTG AGAGAAAATT TTCAGGAAAA AAGACAGTGG | 240 |
| CTCTTGAACT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC  | 300 |
| CATGGTGGGG GTCTTGCATC TGTAAGAATG GAATTGATTT TGCTTTGCA AGAATCTCAG   | 360 |
| CAGGAAACAT CAGAACCACT ATTTTCTAGC CCTCTGTCAAG CAGAAACCTC AGTGCCTCTC | 420 |
| CTCTTTGCTT GT                                                      | 432 |

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACACAACATTG AATAGTAAAA TAGAAACTGA GCTGAAATTT CTAATTCACT TTCTAACCAT | 60  |
| AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTT ATAAAAATTT GT          | 112 |

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

|                                                             |    |
|-------------------------------------------------------------|----|
| ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG | 54 |
|-------------------------------------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ACCTCATTAG TAATTGTTTT GTTGTTCAT TTTTTCTAA TGTCCTCCCT CTACCAGCTC     | 60  |
| ACCTGAGATA ACAGAACATGAA AATGGAAGGA CAGCCAGATT TCTCCTTTGC TCTCTGCTCA | 120 |
| TTCTCTCTGA AGTCTAGGTT ACCCATTTG GGGACCCATT ATAGGCAATA AACACAGTTC    | 180 |
| CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTTCCTTT TCTTAGCCTT    | 240 |
| TTCCTGCAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT   | 300 |
| AGGCTGCCTT CTTTCCATG TCC                                            | 323 |

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACATACATGT GTGTATATTT TTAAATATCA CTTTTGTATC ACTCTGACTT TTTAGCATAAC | 60  |
| TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTCACTC | 120 |

|                                                                  |     |
|------------------------------------------------------------------|-----|
| TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTCAT TTCCCTCAGG TTGGCCAATG | 180 |
| GATAAACAAA GT                                                    | 192 |

## (2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 362 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| CCCTTTTTTA TGGAAATGAGT AGACTGTATG TTTGAANATT TANCCACAAC CTCTTTGACA | 60  |
| TATAATGACG CAACAAAAAG GTGCTGTTA GTCCTATGGT TCAGTTTATG CCCCTGACAA   | 120 |
| GTTCCTTGCCTG ATCTTCTGGC TAATCGGGT ATCCCTCCATG TTATTAGTAA           | 180 |
| TTCTGTATTC CATTGTGTTA ACGCCTGGTA GATGTAACCT GCTANGAGGC TAACCTTATA  | 240 |
| CITATTAAA AGCTCTTATT TTGTGGTCAT TAAAATGGCA ATTATATGTGC AGCACCTTAT  | 300 |
| TGCAGCAGGA AGCACGTGTG GGTTGGTTGT AAAGCTCTTA GCTAATCTTA AAAAGTAATG  | 360 |
| GG                                                                 | 362 |

## (2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 332 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CTTTTTGAAA GATCGTGTCC ACTCCTGTGG ACATCTGTT TTAATGGAGT TTCCCATGCA  | 60  |
| GTANGACTGG TATGGTTGCA GCTGTCCAGA TAAAAACATT TGAAGAGCTC CAAAATGAGA | 120 |
| GTTCCTCCAG GTTCGCCCTG CTGCTCCAAG TCTCAGCAGC AGCCTCTTTT AGGAGGCATC | 180 |
| TTCTGAACTA GATTAAGGCA GCTTGTAAT CTGATGTGAT TTGGTTTATT ATCCAACCAA  | 240 |
| CTTCCATCTG TTATCACTGG AGAAAGCCCA GACTCCCCAN GACNGGTACG GATTGTGGGC | 300 |
| ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT                               | 332 |

## (2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 322 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

|             |            |             |            |            |             |     |
|-------------|------------|-------------|------------|------------|-------------|-----|
| ACTTTTGCCA  | TTTGTATAT  | ATAAACAAATC | TTGGGACATT | CTCCTGAAAA | CTAGGTGTCC  | 60  |
| AGTGGCTAAG  | AGAACTCGAT | TTCAAGCAAT  | TCTGAAAGGA | AAACCAGCAT | GACACAGAAAT | 120 |
| CTCAAATTCC  | CAAACAGGGG | CTCTGTGGGA  | AAAATGAGGG | AGGACCTTTG | TATCTCGGGT  | 180 |
| TTTAGCAAGT  | AAAATGAAN  | ATGACAGGAA  | AGGCTTATT  | ATCAACAAAG | AGAAGAGTTG  | 240 |
| GGATGCTTCT  | AAAAAAAACT | TTGGTAGAGA  | AAATAGGAAT | GCTNAATCCT | AGGGAAAGCCT | 300 |
| GTAAACAATCT | ACAATTGGTC | CA          |            |            |             | 322 |

## (2) INFORMATION FOR SEQ ID NO:133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ACAAGCCTTC  | ACAAGTTAA  | CTAAATTGGG | ATTAATCTT  | CTGTANTTAT | CTGCATAATT | 60  |
| CTTGTGTTTC  | TTTCCATCTG | GCTCCTGGGT | TGACAATTG  | TGGAAACAAC | TCTATTGCTA | 120 |
| CTATTTAAAA  | AAAATCACAA | ATCTTCCCT  | TTAAGCTATG | TTNAATTCAA | ACTATTCTG  | 180 |
| CTATTCCCTGT | TTTGTCAAAG | AAATTATATT | TTTCAAATA  | TGTNTATTG  | TTTGATGGGT | 240 |
| CCCACGAAAC  | ACTAATAAAA | ACCACAGAGA | CCAGCCTG   |            |            | 278 |

## (2) INFORMATION FOR SEQ ID NO:134:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

|            |           |            |            |            |            |     |
|------------|-----------|------------|------------|------------|------------|-----|
| GTTTANAAAA | CTTGTAGC  | TCCATAGAGG | AAAGAATGTT | AAACTTGT   | TTTTAAAACA | 60  |
| TGATTCTCTG | AGGTAAACT | TGGTTTCAA  | ATGTTATT   | TACTTGTATT | TTGCTTTGG  | 120 |
| T          |           |            |            |            |            | 121 |

## (2) INFORMATION FOR SEQ ID NO:135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTTANAACC ATGCCTAGCA CATCAGAAC                                   | 60  |
| ATANCAAGTG GTGACTGGTT AAGCGTGCAG CAAAGTCAG CTGGCACATT ACTTGTGTGC  | 120 |
| AAACATTGATA CTTTTGTTCT AAGTAGGAAC TAGTATACAG TNCTAGGAN TGGTACTCCA | 180 |
| GGGTGCCCGG CAACTCCTGC AGCCGCTCCT CTGTGCCAGN CCCTGNAAGG AACCTTCGCT | 240 |
| CCACCTCAAT CAAGCCCTGG GCCATGCTAC CTGCAATTGG CTGAACAAAC GTTTGCTGAG | 300 |
| TTCCCAAGGA TGCAAAGCCT GGTGCTAAC TCCTGGGGCG TCAACTCAGT             | 350 |

## (2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 399 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TGTACCGTGA AGACGACAGA AGTTGCATGG CAGGGACAGG GCAGGGCCGA GGCCAGGGTT | 60  |
| GCTGTGATTG TATCCGAATA NTCCCTGTGA GAAAAGATAA TGAGATGACG TGAGCAGCCT | 120 |
| GCAGACTTGT GTCTGCCTTC AANAAGCCAG ACAGGAAGGC CCTGCCTGCC TTGGCTCTGA | 180 |
| CCTGGCGGCC AGCCAGCCAG CCACAGGTGG GCTTCTTCCT TTTGTGGTGA CAACNCCAAG | 240 |
| AAAACTGCAG AGGCCAGGG TCAGGTGTNA GTGGGTANGT GACCATAAAA CACCAGGTGC  | 300 |
| TCCCAGGAAC CGGGGCAAAG GCCATCCCCA CCTACAGCCA GCATGCCAC TGGCGTGATG  | 360 |
| GGTGCAGANG GATGAAGCAG CCAGNTGTTG TGCTGTGGT                        | 399 |

## (2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 165 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACTGGGTGTGG TNGGGGGTGA TGCTGGTGGT ANAAGTTGAN GTGACTTCAN GATGGTGTGT | 60  |
| GGAGGAAGTG TGTGAACGTA GGGATGTAGA NGTTTTGGCC GTGCTAAATG AGCTTCGGGA  | 120 |
| TTGGCTGGTC CCACTGGTGG TCACTGTCAT TGGTGGGGTT CCTGT                  | 165 |

## (2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 338 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTCACTGGA ATGCCACATT CACAACAGAA TCAGAGGTCT GTGAAAACAT TAATGGCTCC | 60  |
| TTAACCTCTC CAGTAAGAAT CAGGGACTTG AAATGGAAAC GTTAACAGCC ACATGCCAA  | 120 |
| TGCTGGGCAG TCTCCCATGC CTTCCACAGT GAAAGGGCTT GAGAAAAATC ACATCCAATG | 180 |
| TCATGTGTTT CCAGCCACAC CAAAAGGTGC TTGGGGTGGGA GGGCTGGGG CATANANGT  | 240 |
| CANGCCTAG GAAGCCTCAA GTTCCATTCA GCTTGCAC TGTACATTCC CCATNTTAA     | 300 |
| AAAAACTGAT GCCTTTTTT TTTTTTTTG TAAAATTC                           | 338 |

## (2) INFORMATION FOR SEQ ID NO:139:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGGAATCTTG GTTTTGGCA TCTGGTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAA   | 60  |
| GAAAGGGACT TCGAGTAAGA AGGTGATTG CAGCCAGCCT AGTGCCCCGAA GTGAAGGAGA | 120 |
| ATTCAACACAG ACCTCGTCAT TCCTGGTG AGCCTGGTCG GCTCACCGCC TATCATCTGC  | 180 |
| ATTTGCCTTA CTCAGGTGCT ACCGGACTCT GGCCCCTGAT GTCTGTAGTT TCACAGGATG | 240 |
| CCTTATTGTG CTCCTACACC CCACAGGGCC CCCTACTTCT TCGGATGTGT TTTTAATAAT | 300 |
| GTCAGCTATG TGCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG  | 360 |
| GCCTGGAACT TGTAAAGT GT                                            | 382 |

## (2) INFORMATION FOR SEQ ID NO:140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACCAAANCTT CTTCTGTTG TGTTNGATTT TACTATAGGG GTTTNGCTTN TTCTAAANAT  | 60  |
| ACTTTTCATT TAACANCTTT TGTTAAGTGT CAGGCTGCAC TTTGCTCCAT ANAATTATTG | 120 |
| TTTTCACATT TCAACTTGTA TGTGTTGTC TCTTANAGCA TTGGTGAAAT CACATATTG   | 180 |
| ATATTCAAGCA TAAAGGAGAA                                            | 200 |

## (2) INFORMATION FOR SEQ ID NO:141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACTTTATTTT CAAAACACTC ATATGTTGCA AAAAACACAT AGAAAAATAA AGTTTGGTGG  | 60  |
| GGGTGCTGAC TAAACATTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTTGT  | 120 |
| ATGCATGTAG AGAACCCAAA CTAATTTATT AAACAGGATA GAAACAGGCT GTCTGGGTGA  | 180 |
| AATGGTTCTG AGAACCATCC AATTCACTG TCAGATGCTG ATANACTAGC TCTTCAGATG   | 240 |
| TTTTCTTACG AGTTCAAGAGA TNGGTTAATG ACTANNTCCA ATGGGGAAAA AGCAAGATGG | 300 |
| ATTCAACAAAC CAAGTAATTAAACAAAGA CACTT                               | 335 |

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 459 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACCAGGTTAA TATTGCCACA TATATCCTTT CCAATTGCGG GCTAACAGA CGTGTATTAA   | 60  |
| GGGTTGTTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTCACCTTT CATGGAGTAT  | 120 |
| CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTTTA TTCAGATAGC AGTCTGATCA  | 180 |
| CACATGGTCC AACAAACACTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC | 240 |
| TTCAAACATC ATAGCCAATG ATGCCCCGCT TGCCTATAAT CTCTCCGACA TAAAACCACA  | 300 |
| TCAACACCTC AGTGGCCACC AAACCAATTCA GCACAGCTTC CTTAACTGTG AGCTGTTGA  | 360 |
| AGCTACCAGT CTGAGCACTA TTGACTATNT TTTTCANGCT CTGAATAGCT CTAGGGATCT  | 420 |
| CAGCANGGGT GGGAGGAACC AGCTCAACCT TGGCGTANT                         | 459 |

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACATTTCCTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG | 60  |
| AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTACCA ACCCCACCCA TCTCCCTGAG  | 120 |
| ACCATCCGAC TTCCCTGTGT                                             | 140 |

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 164 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| ACTTCAGTAA CAACATACAA TAACAACATT AAGTGTATAT TGCCATCTTT GTCATTTCT | 60  |
| ATCTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTG | 120 |
| AGGCAATTAA TCCATATTG TTTTCAATAA GGAAAAAAAG ATGT                  | 164 |

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 303 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACGTAGACCA TCCAACTTTG TATTTGTAAT GGCAAACATC CAGNAGCAAT TCCTAAACAA | 60  |
| ACTGGAGGGT ATTATACCC AATTATCCA TTCATTAACA TGCCCTCCTC CTCAGGCTAT   | 120 |
| GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTGAT ATAAACTTCA  | 180 |
| GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGG GAAATGGAAC ATAAGCCAG   | 240 |
| TAGTAAAATN TTGCTTAGCT GAAACAGCCA CAAAAGACTT ACCGCCGTGG TGATTACCAT | 300 |
| CAA                                                               | 303 |

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTGCAGCTC AATTAGAAGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC | 60  |
| ACTGGCCTGG AGTGACTCAT TGCTCTGGTT GGTTGAGAGA GCTCCTTGC CAACAGGCT   | 120 |
| CCAAGTCAGG GCTGGGATTG GTTCTCTTC CACATTCTAG CAACAATATG CTGGCCACTT  | 180 |
| CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGGAACAAGC TGCCACTTTC TAAAGTAGCC | 240 |
| AGACTTGGCC CTGGGCTGT CACACCTACT GATGACCTTC TGTGCTGCA GGATGGAATG   | 300 |
| TAGGGGTGAG CTGTGTGACT CTATGGT                                     | 327 |

## (2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 173 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACATTGTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG  | 60  |
| ACTGGAACAC ATACCCACAT CTTTGTTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT | 120 |
| ATATTCAAGC ACATATGTIA TATATTATTC AGTTCATGT TTATAGCCTA GTT         | 173 |

## (2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 477 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACAACCACIT TATCTCATCG AATTTTAAC CCAAACTCAC TCACTGTGCC TTTCTATCCT   | 60  |
| ATGGGATATA TTATTTGATG CTCCATTCTA TCACACATAT ATGAATAATA CACTCATACT  | 120 |
| GCCCTACTAC CTGCTGCAAT AACACATTC CCTTCCTGTC CTGACCCCTGA AGCCATTGGG  | 180 |
| GTGGTCCTAG GTGCCATCAG TCCANGCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC   | 240 |
| NCCANCCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC CTCCCTGCTC TCTAACCCCCA | 300 |
| TAGATTATNT CCAAATTCAAG TCAATTAAGT TACTATTAAC ACTCTACCCG ACATGTCCAG | 360 |
| CACCACTGGT AAGCCTTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT  | 420 |
| CCAGGCACAG GCTACCTCAT CTTCACAATC ACCCCTTAA TTACCATGCT ATGGTGG      | 477 |

## (2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 207 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTTAAG AGGGAAGAAC | 60  |
| TAACGTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCCT | 120 |

|                                                                  |     |
|------------------------------------------------------------------|-----|
| GATGATAAAT AAGAGTCAGC CAGGTAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAAC | 180 |
| TTTCAGGCAG AGGAAACAGC AGTGAAA                                    | 207 |

## (2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGG | 60  |
| CACTTAAATG TGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTTGGG T          | 111 |

## (2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGCGCGGCAG GTCATATTGA ACATTCAGA TACCTATCAT TACTCGATGC TGTTGATAAC  | 60  |
| AGCAAGATGG CTTTGAACTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT | 120 |
| GGATACCAAC CGAAAAACCC CTATCCCGCA CAGCCCCTG TGTCCCCCAC TGTCTACGAG  | 180 |
| GTGCATCCGG CTCAGT                                                 | 196 |

## (2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC   | 60  |
| CTTCCCCCTTT TCATCTAGTG GTGGAAACCT GATGCTTTAT GTTGACAGGA ATAGAACCCAG | 120 |
| GAGGGAGTTT GT                                                       | 132 |

## (2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 285 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ACAAANACCCA NGANAGGCCA CTGGCCGTGG TGTCAATGCC TCCAACATG AAAGTGTCA    | 60  |
| CTTCCTGCTCT TATGTCCCTCA TCTGACAACCT CTTTACCATT TTATCCTCG CTCAGCAGGA | 120 |
| GCACATCAAT AAAGTCCAAA GTCTTGGACT TGGCCTTGGC TTGGAGGAAG TCATCAACAC   | 180 |
| CCTGGCTAGT GAGGGTGCGG CGCCGCTCCT GGATGACGGC ATCTGTGAAG TCGTGCACCA   | 240 |
| GTCTGCAGGC CCTGTGGAAG CGCCGCTCAC ACGGAGTNAG GAATT                   | 285 |

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACACAGTCC TGGTGGGCCA GGGCTTCATG ACCCTTTCTG TGAAAAGCCA TATTATCACC  | 60  |
| ACCCCAAATT TTTCCTTAAA TATCTTTAAC TGAAGGGTC AGCCTCTTGA CTGCAAAGAC  | 120 |
| CCTAACCGGG TTACACAGCT AACTCCCACT GGCCCTGATT TGTGAAATTG CTGCTGCC   | 180 |
| ATTGGCACAG GAGTCGAAGG TGTTCAGCTC CCCTCCTCCG TGGAACGAGA CTCTGATTG  | 240 |
| AGTTTACCAA ATTCTCGGGC CACCTCGTCA TTGCTCCTCT GAAATAAAAT CGGGAGAATG | 300 |
| GTCAGGCCTG TCTCATCCAT ATGGATCTTC CGG                              | 333 |

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAA GATCATCAGG GCATGGATGG  | 60  |
| GAAAGTGCTT TGGGAACTGT AAAGTGCTTA ACACATGATC GATGATTTTT GTTATAATAT | 120 |
| TTGAATCACG GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGGCCCCAG CCCCAGCCCC | 180 |
| ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTTGGCT | 240 |

|                                                                  |     |
|------------------------------------------------------------------|-----|
| GCTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGT AAGGCATGCTG | 300 |
| GCCCTGGT                                                         | 308 |

## (2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACCTTGCTCG GTGCTTGGAA CATAATTAGGA ACTCAAAATA TGAGATGATA ACAGTGCCTA | 60  |
| TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAACTGA  | 120 |
| GAATAGGAGA TTATGTTGG CCCTCATATT CTCTCCTATC CTCCCTTGCT CATTCTATGT   | 180 |
| CTAATATATT CTCATCCTAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT  | 240 |
| AAAACCAGAT GTCTATCCTT AAGATTTCA AATAGAAAAAC AAATTAACAG ACTAT       | 295 |

## (2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACAAGTTAA ATAGTGCTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTCT    | 60  |
| GAAGAGCAAA ACAAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGGTA TATCTGTCCC | 120 |
| CTTAGT                                                             | 126 |

## (2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACCCACTGGT CTTGGAAACA CCCATCCTTA ATACGATGAT TTTTCTGTG TGTAAGATG    | 60  |
| AANCCAGCAG GCTGCCCTA GTCAGTCCTT CCTTCCAGAG AAAAAGAGAT TTGAGAAAGT   | 120 |
| GCCTGGGTA TTCACCATTAA ATTTCTCCCC CCAAACCTCTC TGAGTCTTCC CTTAATATTT | 180 |

100

|             |            |              |            |            |            |     |
|-------------|------------|--------------|------------|------------|------------|-----|
| CTGGTGGTTC  | TGACCAAAGC | AGGTCAATGGT  | TTGTTGAGCA | TTTGGGATCC | CAGTGAAGTA | 240 |
| NATGTTGTA   | GCCTTGATA  | CTTAGCCCCCTT | CCCACGCACA | AACGGAGTGG | CAGAGTGGTG | 300 |
| CCAACCCCTGT | TTTCCCAGTC | CACGTAGACCA  | GATTCACAGT | GCGGAATTCT | GGAAGCTGGA | 360 |
| NACAGACGGG  | CTCTTTGAG  | AGCCGGACT    | CTGAGANGGA | CATGAGGGCC | TCTGCCTCTG | 420 |
| TGTTCATCT   | CTGATGTCCT | GT           |            |            |            | 442 |

## (2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

|             |             |             |             |            |             |     |
|-------------|-------------|-------------|-------------|------------|-------------|-----|
| ACTTCCAGGT  | AACGTTGTTG  | TTTCCGTTGA  | GCCTGAACTG  | ATGGGTGACG | TTGTAGGTTTC | 60  |
| TCCAACAAGA  | ACTGAGGTTG  | CAGAGCGGGT  | AGGGAAAGAGT | GCTGTTCCAG | TTGCACCTGG  | 120 |
| GCTGCTGTGG  | ACTGTTGTTG  | ATTCCTCACT  | ACGGCCCAAG  | GTTGTGGAAC | TGGCANAAAG  | 180 |
| GTGTGTTGTT  | GGANTTGGAC  | TCGGGCGGCT  | GTGGTAGGTT  | GTGGGCTCTT | CAACAGGGGC  | 240 |
| TGCTGTTGTT  | CCGGGANGTG  | AANGTGTGTTG | GTCACCTGAG  | CTTGGCCAGC | TCTGGAAAGT  | 300 |
| ANTANATTCT  | TCTCTGAAGGC | CAGCGCTTGT  | GGAGCTGGCA  | NGGGTCANTG | TTGTGTGTA   | 360 |
| CGAACCGATG  | CTGCTGTGGG  | TGGGTGTANA  | TCCTCCACAA  | AGCCTGAAGT | TATGGTGTGN  | 420 |
| TCAGGTAANA  | ATGTGGTTTC  | AGTGTCCCTG  | GGCNGCTGTG  | GAAGGTTGTA | NATTGTCAACC | 480 |
| AAGGGAAATAA | GCTGTGGT    |             |             |            |             | 498 |

## (2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| ACCTGCATCC | AGCTTCCCTG | CCAAACTCAC | AAGGAGACAT  | CAACCTCTAG  | ACAGGGAAAC | 60  |
| AGCTTCAGGA | TACTTCCAGG | AGACAGAGCC | ACCAGCAGCA  | AAACAAATAT  | TCCCATGCCT | 120 |
| GGAGCATGGC | ATAGAGGAAG | CTGANAAATG | TGGGGTCTGA  | GGAAAGCCATT | TGAGTCTGGC | 180 |
| CACTAGACAT | CTCATCAGCC | ACTTGTGTGA | AGAGATGCC   | CATGACCCCCA | GATGCCTCTC | 240 |
| CCACCCCTAC | CTCCATCTCA | CACACTTGAG | CTTTCACACT  | TGTATAATTG  | TAACATCCTG | 300 |
| GAGAAAATG  | GCAGTTTGAC | CGAACCTGTT | CACAAACGGTA | GAGGCTGATT  | TCTAACGAAA | 360 |
| CTTGTAGAAT | GAAGCCTGGA |            |             |             |            | 380 |

## (2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTCCACATC CCCTCTGAGC AGGCGGTTGT CGTTCAAGGT GTATTTGGCC TTGCCTGTCA | 60  |
| CACTGTCCAC TGGCCCCTTA TCCACTTGGT GCTTAATCCC TCGAAAGAGC ATGT       | 114 |

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACTTTCTGAA TCGAATCAA TGATACTTAG TGTAGTTTA ATATCCTCAT ATATATCAA  | 60  |
| GTTTACTAC TCTGATAATT TTGTAAACCA GGTAACCAGA ACATCCAGTC ATACAGCTT | 120 |
| TGGTGATATA TAACTTGGCA ATAACCCAGT CTGGTGATAC ATAAAACATAC TCACGT  | 177 |

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| CATTTATACA GACAGGGCGTG AAGACATTCA CGACAAAAAAC GCGAAATTCT ATCCCGTGAC | 60  |
| CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT   | 120 |
| CATCAGCGGC ATGATGT                                                  | 137 |

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTA    | 60  |
| TGCAATGCAT CATGCTATT CATACTAAT GAGGGAGTTC CAGGAGATTG AACCCAGGAAA    | 120 |
| TGCATGGATC TCAAAGGAAA CAAACACCCA ATAAACTCGG AGTGGCAGAC TGACAACTGT   | 180 |
| GAGACATGCA CTTGCTACGA AACAGAAAATT TCATGTTGCA CCCTTGTTTC TACACCTGTG  | 240 |
| GGTTATGACA AAGACAACTG CCAAAGAACATC TTCAAGAAGG AGGACTGCAA GTATATCGTG | 300 |
| GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCAGTG AATGGATAAT CTAATGTGCT   | 360 |
| TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT   | 420 |
| GATTGTGTAG CCATGCCTAT CAGTAAAAAG ATNTTGAGC AAACACTTT                | 469 |

## (2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 195 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| ACAGTTTTT ATANATATCG ACAITGCCGG CACTTGTGTT CAGTTTCATA AAGCTGGTGG | 60  |
| ATCCGCTGTC ATCCACTATT CCTTGGCTAG AGTAAAATT ATTCTTATAG CCCATGTCCC | 120 |
| TGCAGGCCGC CGCCCGCTAG TTCTCGTTC AGTCGTCTG GCACACAGGG TGCCAGGACT  | 180 |
| TCCTCTGAGA TGAGT                                                 | 195 |

## (2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ACATCTTAGT AGTGTGGCAC ATCAGGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC   | 60  |
| CGAGGTGCGGA GTCCACACCA CCGGTGTTAGG TGTGCTCAAT CTTGGGCTTG GCGCCCACCT | 120 |
| TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAACCTG CCAAAGAATT   | 180 |
| TTTGCAAGACC AGCCTGAGCA AGGGGCGGAT GTTCAGCTTC AGTCCTCCT TCGTCAGGTG   | 240 |
| GATGCCAACC TCGTCTANGG TCCGTGGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGGC   | 300 |
| GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCCACGAAA CTTCTCTGGG AGCTGCTAGT   | 360 |
| NGGGGCCTTT TTGGTGAAC TTC                                            | 383 |

## (2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 247 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT | 60  |
| TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC | 120 |
| TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC | 180 |
| TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC | 240 |
| TGANGTC                                                           | 247 |

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACTTCTAAGT TTTCTAGAAG TCCAAGGATT GTANTCATCC TGAAAATGGG TTTACTTCAA  | 60  |
| AATCCCTCAN CCTTGTTCTT CACNACTGTC TATACTGANA GTGTCACTGTT TCCACAAAGG | 120 |
| GCTGACACCT GAGCCTGNAT TTTCACTCAT CCCTGAGAAG CCCTTTCCAG TAGGGTGGC   | 180 |
| AATTCCCAAC TTCCCTGCCA CAAGCTTCCC AGGCTTCTC CCCTGGAAAA CTCCAGCTTG   | 240 |
| AGTCCCGAGAT ACACTCATGG GCTGCCCTGG GCA                              | 273 |

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ACAGCCTTGG CTTCCCCAAA CTCCACAGTC TCAGTGCAGA AAGATCATCT TCCAGCAGTC   | 60  |
| AGCTCAGACC AGGGTCAAAG GATGTGACAT CAACAGTTTC TGGTTTCAGA ACAGGTTCTA   | 120 |
| CTACTGTCAA ATGACCCCCC ATACTTCCTC AAAGGCTGTG GTAAGTTTG CACAGGTGAG    | 180 |
| GGCAGCAGAA AGGGGGTANT TACTGTGGA CACCATCTTC TCTGTATACT CCACACTGAC    | 240 |
| CTTGCCATGG GCAAAGGCCCT ACCACACAAA AACAAATAGGA TCACTGCTGG GCACCAGCTC | 300 |
| ACGCACATCA CTGACAACCG GGATGGAAA AGAANTGCCA ACTTTCATAC ATCCAACCTGG   | 360 |
| AAAGTGATCT GATACTGGAT TCTTAATTAC CTTCAAAAGC TTCTGGGGC CATCAGCTGC    | 420 |
| TCGAACACTG.A                                                        | 431 |

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACCTGTGGC TGGGCTGTTA TGCCCTGTGCC GGCTGCTGAA AGGGAGTTCA GAGGTGGAGC | 60  |
| TCAAGGAGCT CTGCAGGCAT TTTGCCAACCTCTCCANAG CANAGGGAGC AACCTACACT   | 120 |
| CCCCGCTAGA AAGACACCAG ATTGGAGTCC TGGGAGGGGG AGTTGGGGTG GGCATTGAT  | 180 |
| GTATACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT | 240 |
| TCAAAGCTAG GGGTCTGGCA GGTGGA                                      | 266 |

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

|                                                                     |      |
|---------------------------------------------------------------------|------|
| GGCAGCCAAA TCATAAACCGG CGAGGACTGC AGCCCCACT CGCAGCCCTG GCAGGCGGCA   | 60   |
| CTGGTCATGG AAAACGAATT GTTCTGCTCG GGCGTCTGG TGCACTCGCA GTGGGTGCTG    | 120  |
| TCAGCCGCAC ACTGTTTCCA GAAGTGAGTG CAGAGCTCT ACACCATCGG GCTGGGCTG     | 180  |
| CACAGTCITG AGGCCGACCA AGAGCCAGGG AGCCAGATGG TGGAGGCCAG CCTCTCCGTA   | 240  |
| CGGCACCCAG AGTACAACAG ACCCTTGCTC GCTAACGCCAC TCATGCTCAT CAAGTTGGAC  | 300  |
| GAATCCGTGT CCCAGTCTGA CACCATCCGG AGCATCAGCA TTGCTTCGCA GTGCCCTTAC   | 360  |
| GCGGGGAACCT CTTGGCTCGT TTCTGGCTGG GGTCTGCTGG CGAACGGCAG AATGCCCTACC | 420  |
| GTGCTGCAGT GCGTGAACGT GTCCGGTGGTG TCTGAGGAGG TCTGCACTAA GCTCTATGAC  | 480  |
| CCGCTGTACC ACCCCAGCAT GTTCTGCGCC GGCAGGGGGC AAGACCCAGAA GGACTCCTGC  | 540  |
| AACGGTGACT CTGGGGGGCC CCTGATCTGC AACGGGTACT TGCAAGGGCT TGTGTCTTTC   | 600  |
| GGAAAAGCCC CGTGTGGCCA AGTTGGCTG CCAGGTGTCT ACACCAACCT CTGCAAATT     | 660  |
| ACTGAGTGA TAGAGAAAAC CGTCCAGGGCC AGTTAACTCT GGGGACTGGG AACCCATGAA   | 720  |
| ATTGACCCCC AAATACATCC TGCGGAAGGA ATTCAAGGAAT ATCTGTTCCC AGCCCCCTCC  | 780  |
| CCCTCAGGCC CAGGAGTCCA GGCCCCCAGC CCCTCCCTCC TCAAAACCAAG GGTACAGATC  | 840  |
| CCCAGCCCCCT CCTCCCTCAG ACCCAGGAGT CCAGACCCCC CAGCCCCCTCC TCCCTCAGAC | 900  |
| CCAGGAGTCC AGCCCCCTCC CCCTCAGACC CAGGAGTCCA GACCCCCCAG CCCCTCCCTCC  | 960  |
| CTCAGACCCA GGGGTCCAGG CCCCCAACCC CTCCCTCCCTC AGACTCAGAG GTCCAAGCCC  | 1020 |
| CCAACCCNTC ATTCCCCAGA CCCAGAGGTC CAGGTCCAG CCCTCTNCCT CTCAGACCCA    | 1080 |
| GCGGTCCAAT GCCACCTAGA CTNTCCCTGT ACACAGTGC CCCTTGTGGC ACGTTGACCC    | 1140 |
| AACCTTACCA GTTGGTTTTT CATTNTNGT CCCTTCCCC TAGATCCAGA AATAAAAGTTT    | 1200 |
| AAGAGAAGNG CAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA                      | 1248 |

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Glu | Ala | Ser | Leu | Ser | Val | Arg | His | Pro | Glu | Tyr | Asn | Arg | Pro |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Leu | Leu | Ala | Asn | Asp | Leu | Met | Leu | Ile | Lys | Leu | Asp | Glu | Ser | Val | Ser |
|     |     |     |     |     | 20  |     |     | 25  |     |     |     |     | 30  |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Glu | Ser | Asp | Thr | Ile | Arg | Ser | Ile | Ser | Ile | Ala | Ser | Gln | Cys | Pro | Thr |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ala | Gly | Asn | Ser | Cys | Leu | Val | Ser | Gly | Trp | Gly | Leu | Leu | Ala | Asn | Gly |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Arg | Met | Pro | Thr | Val | Leu | Gln | Cys | Val | Asn | Val | Ser | Val | Val | Ser | Glu |
|     |     |     |     | 65  |     |     | 70  |     |     | 75  |     |     | 80  |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Glu | Val | Cys | Ser | Lys | Leu | Tyr | Asp | Pro | Leu | Tyr | His | Pro | Ser | Met | Phe |
|     |     |     |     | 85  |     |     | 90  |     |     |     |     | 95  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Cys | Ala | Gly | Gly | Gly | Gln | Xaa | Gln | Xaa | Asp | Ser | Cys | Asn | Gly | Asp | Ser |
|     |     |     |     | 100 |     |     | 105 |     |     |     |     | 110 |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gly | Gly | Pro | Leu | Ile | Cys | Asn | Gly | Tyr | Leu | Gln | Gly | Leu | Val | Ser | Phe |
|     |     |     |     | 115 |     |     | 120 |     |     |     | 125 |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gly | Lys | Ala | Pro | Cys | Gly | Gln | Val | Gly | Val | Pro | Gly | Val | Tyr | Thr | Asn |
|     |     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Leu | Cys | Lys | Phe | Thr | Glu | Trp | Ile | Glu | Lys | Thr | Val | Gln | Ala | Ser |     |
|     |     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1265 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| GGCAGCCCGC | ACTCGCAGGCC | CTGGCAGGCG | GCACCTGGTCA | TGGAAAACGA | ATTGTTCTGC | 60  |
| TCGGGCGTCC | TGGTGCATCC  | GCAGTGGGTG | CTGTCAGCCG  | CACACTGTTT | CCAGAACTCC | 120 |
| TACACCATCG | GGCTGGGCCT  | GCACAGTCTT | GAGGCCGACC  | AAGAGCCAGG | GAGCCAGATG | 180 |
| GTGGAGGCCA | GCCTCTCCGT  | ACGGCACCCA | GAGTACAACA  | GACCCTTGCT | CGCTAACGAC | 240 |

|            |             |             |             |             |              |      |
|------------|-------------|-------------|-------------|-------------|--------------|------|
| CTCATGCTCA | TCAAGTTGGA  | CGAATCCGTG  | TCGGAGTCTG  | ACACCACATCG | GAGCATTACAGC | 300  |
| ATTGCTTCGC | AGTGCCCTAC  | CGCGGGAAAC  | TCTTGCTCG   | TTTCTGGCTG  | GGGTCTGCTG   | 360  |
| GCGAACGGTG | AGCTCACGGG  | TGTGTGCTG   | CCCTCTTCAA  | GGAGGGTCTC  | TGCCCAGTCG   | 420  |
| CGGGGGCTGA | CCCAGAGCTC  | TGCGTCCCAG  | GCAGAATGCC  | TACCGTGTG   | CAGTGCCTGA   | 480  |
| ACGTGTCGGT | GGTGTCTGAG  | GAGGTCTGCA  | GTAAGCTCTA  | IGACCCGCTG  | TACCAACCCA   | 540  |
| GCATGTTCTG | CGCCGGCGGA  | GGGCAAGACC  | AGAAGGACTC  | CTGCAACGGT  | GACTCTGGGG   | 600  |
| GGCCCCGTAT | CTGCAACGGG  | TACTTGCAGG  | GCCTTGTGTC  | TTTCGGAAAA  | GGCCCGTGTG   | 660  |
| GCCAAGTTGG | CGTGCCAGGT  | GTCTACACCA  | ACCTCTGCAA  | ATTCACTGAG  | TGGATAGAGA   | 720  |
| AAACCGTCCA | GGCCAGTTAA  | CTCTGGGAC   | TGGGAACCCA  | TGAAATTGAC  | CCCCAAATAC   | 780  |
| ATCCTGCGGA | AGGAATTCA   | GAATATCTGT  | TCCCAGCCCC  | TCCTCCCTCA  | GGCCCGAGGAG  | 840  |
| TCCAGGCCCC | CAGCCCCCTCC | TCCCTCAAAC  | CAAGGGTACA  | GATCCCCAGC  | CCCTCCCTCCC  | 900  |
| TCAGACCCAG | GAGTCCAGAC  | CCCCCAGCCC  | CTCCTCCCTC  | AGACCCAGGA  | GTCCAGCCCC   | 960  |
| TCCTCCNTCA | GACCCAGGAG  | TCCAGACCCC  | CCAGCCCCCTC | CTCCCTCAGA  | CCCAAGGGTT   | 1020 |
| GAGGGCCCCA | ACCCCTCCTC  | CTTCAGAGTC  | AGAGGTCCAA  | GCCCCCAACC  | CCTCGTTCCC   | 1080 |
| CAGACCCAGA | GGTNNNAGGTC | CCAGCCCCCTC | TTCCNTCAGA  | CCCAGNGGTC  | CAATGCCACC   | 1140 |
| TAGATTTTCC | CTGNACACAG  | TGCCCCCTTG  | TGGNANGTTG  | ACCCAACCTT  | ACCAAGTTGGT  | 1200 |
| TTTTCATTTT | TNGTCCCTTT  | CCCTAGATC   | CAGAAATAAA  | GTGAAAGAGA  | NGNGCAAAAA   | 1260 |
| AAAAAA     |             |             |             |             |              | 1265 |

## (2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1459 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

|                     |             |             |             |             |             |      |
|---------------------|-------------|-------------|-------------|-------------|-------------|------|
| GGTCAGCCGC          | ACACTGTTTC  | CAGAAGTGAG  | TGCAGAGCTC  | CTACACCATC  | GGGCTGGGCC  | 60   |
| TGCACAGTCT          | TGAGGCCGAC  | CAAGAGCCAG  | GGAGCCAGAT  | GGTGGAGGCC  | AGCCCTCTCCG | 120  |
| TACGGCACCC          | AGAGTACAAC  | AGACCCCTTGC | TCGCTAACGA  | CCTCATGCTC  | ATCAAGTTGG  | 180  |
| ACGAATCCGT          | GTCCGAGTCT  | GACACCATTCC | GGAGCATCAG  | CATTGCTTCG  | CAGTGCCTTA  | 240  |
| CCGGGGGAA           | CTCTTGCCCTC | GTTCCTGGCT  | GGGGTCTGCT  | GGCGAACGGT  | GAGCTCACGG  | 300  |
| GTGTGTGTC           | GGCCCTCTTC  | AGGAGGTCTC  | CTGCCAGTC   | GGGGGGCTG   | ACCCAGAGCT  | 360  |
| CTGCGTCCA           | GGCAGAAATGC | CTACCGTGTG  | GCAGTGCCTG  | AACGTGTGCG  | TGGTGTCTGA  | 420  |
| NGAGGTCTGC          | ANTAACGCTCT | ATGACCCGGT  | GTACCAACCCC | ANCATGTTCT  | GGCCGGCGG   | 480  |
| AGGGCAAGAC          | CAGAAGGACT  | CCTGCAACGT  | GAGAGAGGGG  | AAAGGGGAGG  | GCAGGCAGT   | 540  |
| CAGGGAAAGG          | TGAGGAAGGG  | GGAGACAGAG  | ACACACAGGG  | CCGCATGGCG  | AGATGCAGAG  | 600  |
| ATGGAGAGAC          | ACACAGGGAG  | ACAGTGACAA  | CTAGAGAGAG  | AAACTGAGAG  | AAACAGAGAA  | 660  |
| ATAAACACAG          | GAATAAAAGAG | AAGCAAAGGA  | AGAGAGAAAC  | AGAAAACAGAC | ATGGGGAGGC  | 720  |
| AGAAACACAC          | ACACATAGAA  | ATGCAGTTGA  | CCTTCCAACA  | GCATGGGCC   | TGAGGGCGGT  | 780  |
| GACCTCCACC          | CAATAGAAAA  | TCCTCTTATA  | ACTTTTGACT  | CCCCAAAAAC  | CTGACTAGAA  | 840  |
| ATAGCCTACT          | GTGACGGGG   | AGCCTTACCA  | ATAACATAAA  | TAGTCGATTT  | ATGCATACT   | 900  |
| TTTATGCTT           | CATGATATAC  | CTTTGTTGGA  | ATTTTTGAT   | ATTTCATAAGC | TACACAGTTC  | 960  |
| GTCTGTGAAT          | TTTTTAAAT   | TGTTGCAACT  | CTCCTAAAT   | TTTCTGTATG  | TGTTTATTGA  | 1020 |
| AAAAATCCAA          | GTATAAGTGG  | ACTTGTGCAT  | TCAAACCAGG  | GTTGTTCAAG  | GGTCAACTGT  | 1080 |
| GTACCCAGAG          | GGAAACAGTG  | ACACAGATTC  | ATAGAGGTGA  | AACACGAAGA  | GGAAACAGGAA | 1140 |
| AAATCAAGAC          | TCTACAAAGA  | GGCTGGGCAG  | GGTGGCTCAT  | GCCTGTAATC  | CCAGCACTTT  | 1200 |
| GGGAGGGCAG          | GCAGGCAGAT  | CACTTGAGGT  | AAGGAGTTCA  | AGACCAGCCT  | GGCCAAAATG  | 1260 |
| GTGAAATCCT          | GTCTGTACTA  | AAAATACAAA  | AGTTAGCTGG  | ATATGGTGGC  | AGGCGCCTGT  | 1320 |
| AATCCCAGCT          | ACTTGGGAGG  | CTGAGGCAGG  | AGAATTGCTT  | GAATATGGGA  | GGCAGAGGTT  | 1380 |
| GAAGTGAGTT          | GAGATCACAC  | CACTATACTC  | CAGCTGGGCC  | AACAGAGTAA  | GACTCTGTCT  | 1440 |
| AAAAAAAAA AAAAAAAAA |             |             |             |             |             | 1459 |

## (2) INFORMATION FOR SEQ ID NO:175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

|             |             |            |            |             |             |      |
|-------------|-------------|------------|------------|-------------|-------------|------|
| GGCGAGCCCT  | GGCAGGCGGC  | ACTGGTCATG | GAAAACGAAT | TGTCTCTGCTC | GGGCGTCCTG  | 60   |
| GTGCATCCGC  | AGTGGGTGCT  | GTCAGCCGCA | CACTGTTTCC | AGAACTCCTA  | CACCATCGGG  | 120  |
| CTGGGCCTGC  | ACAGTCTTGA  | GGCCGACCAA | GAGCCAGGGA | GCCAGATGGT  | GGAGGGCCAGC | 180  |
| CTCTCCGTAC  | GGCACCCAGA  | GTACAACAGA | CTCTTGCTCG | CTAACGACCT  | CATGCTCATC  | 240  |
| AAAGTGGACG  | AATCCGTGTC  | CGAGTCTGAC | ACCATCCGGA | GCATCAGCAT  | TGCTTCCGAG  | 300  |
| TGCCCTACCG  | CGGGGAACTC  | TTGCCCTCGT | TCTGGCTGGG | GTCCTGCTGGC | GAACGGCAGA  | 360  |
| ATGCTTACCG  | TGCTGCACTG  | CGTGAACGTG | TCGGTGGTGT | CTGAGGANGT  | CTGCAGTAAG  | 420  |
| CTCTATGACC  | CGCTGTACCA  | CCCCAGCATG | TTCTGCGCCG | GCGGAGGGCA  | AGACCAGAAG  | 480  |
| GACTCTGCA   | ACGGTGAECT  | TGGGGGCC   | CTGATCTGCA | ACGGGTACTT  | GCAGGGCCTT  | 540  |
| GTGTCTTCG   | AAAAAGCCCC  | GTGTGGCAA  | CTTGGCGTGC | CAGGTGTCTA  | CACCAACCTC  | 600  |
| TGCAAAATTCA | CTGAGTGGAT  | AGAGAAAACC | GTCCAGNCCA | GTAACTCTG   | GGGACTGGGA  | 660  |
| ACCCATGAAA  | TTGACCCCCA  | AATACATCCT | GCGGAANGAA | TTCAGGAATA  | TCTGTTCCCA  | 720  |
| GCCCCCTCTC  | CCTCAGGCC   | AGGAGTCCAG | GCCCCCAGCC | CCTCCTCCCT  | CAAACCAAGG  | 780  |
| GTACAGATCC  | CCAGCCCCCTC | CTCCCTCAGA | CCCAGGAGTC | CAGACCCCCC  | AGCCCCCTCNT | 840  |
| CCNTCAGACC  | CAGGAGTCCA  | GCCCCCTCTC | CNTCAGACGC | AGGAGTCCAG  | ACCCCCCAGC  | 900  |
| CCNTCNTCCG  | TCAGACCCAG  | GGGTGCAGGC | CCCCAACCCC | TCNTCCNTCA  | GAGTCAGAGG  | 960  |
| TCCAAGCCCC  | CAACCCCTCG  | TTCCCCAGAC | CCAGAGGTNC | AGGTCCCAGC  | CCCTCCTCCC  | 1020 |
| TCAGACCCAG  | CGGTCCAATG  | CCACCTAGAN | TNTCCCTGTA | CACAGTGGCC  | CCTTGTGGCA  | 1080 |
| NGTTGACCCA  | ACCTTACCAAG | TTGGTTTTTC | ATTTTTGTC  | CCTTTCCCT   | AGATCCAGAA  | 1140 |
| ATAAAGNTA   | AGAGAAGCGC  | AAAAAAA    |            |             |             | 1167 |

(2) INFORMATION FOR SEQ ID NO:176:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asn | Glu | Leu | Phe | Cys | Ser | Gly | Val | Leu | Val | His | Pro | Gln | Trp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     | 15  |     |     |     |
| Val | Leu | Ser | Ala | Ala | His | Cys | Phe | Gln | Asn | Ser | Tyr | Thr | Ile | Gly | Leu |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     | 30  |     |     |     |
| Gly | Leu | His | Ser | Leu | Glu | Ala | Asp | Gln | Glu | Pro | Gly | Ser | Gln | Met | Val |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     | 45  |     |     |     |
| Glu | Ala | Ser | Leu | Ser | Val | Arg | His | Pro | Glu | Tyr | Asn | Arg | Leu | Leu |     |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     | 60  |     |     |     |

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser  
 65                    70                    75                    80  
  
 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly  
 85                    90                    95  
  
 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met  
 100                  105                  110  
  
 Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val  
 115                  120                  125  
  
 Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala  
 130                  135                  140  
  
 Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly  
 145                  150                  155                  160  
  
 Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys  
 165                  170                  175  
  
 Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys  
 180                  185                  190  
  
 Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser  
 195                  200                  205

## (2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

|             |            |             |             |            |            |      |
|-------------|------------|-------------|-------------|------------|------------|------|
| GGCGCACTCGC | AGCCCTGGCA | GGCGGCACTG  | GTCATGGAAA  | ACGAATTGTT | CTGCTCGGGC | 60   |
| GTCCTGGTGC  | ATCCGCAGTG | GGTGTGTCA   | GCCGCACACT  | GTTTCCAGAA | CTCCTACACC | 120  |
| ATCAGGGCTGG | GCCTGCACAG | TCTTGAGGCC  | GACCAAGAGC  | CAGGGAGGCC | GATGGTGGAG | 180  |
| GCCAGCCTCT  | CCGTACGGCA | CCCAGAGTAC  | AACAGACCCCT | TGCTCGCTAA | CGACCTCATG | 240  |
| CTCATCAAGT  | TGGACGAATC | CGTGTCCGAG  | TCTGACACCA  | TCCGGAGCAT | CAGCATTGCT | 300  |
| TCGCAGTGCC  | CTACCGCGGG | GAACCTTGTG  | CTCGTTTCTG  | GCTGGGGTCT | GCTGGCGAAC | 360  |
| GATGCTGTGA  | TTGCCATCCA | GTCCCAGACT  | GTGGGAGGCT  | GGGAGTGTGA | GAAGCTTTC  | 420  |
| CAACCCCTGGC | AGGGTTGTAC | CATTTCCGCA  | ACTTCCAGTG  | CAAGGACGTC | CTGCTGCATC | 480  |
| CTCACTGGGT  | GCTCACTACT | GCTCACTGCA  | TCACCCGGAA  | CACTGTGATC | AACTAGCCAG | 540  |
| CACCATAGTT  | CTCCGAAGTC | AGACTATCAT  | GATTACTGTG  | TTGACTGTGC | TGTCTATTGT | 600  |
| ACTAACCATG  | CCGATGTTTA | GGTGAAATTA  | GCGTCACTTG  | GCCTCAACCA | TCTTGGTATC | 660  |
| CAGTTATCCT  | CACTGAATTG | AGATTTCTG   | CTTCAGTGTG  | AGCCATTCCC | ACATAATTTC | 720  |
| TGACCTACAG  | AGGTGAGGG  | TCATATAAGCT | CTTCAAGGAT  | GCTGGTACTC | CCCTCACAAA | 780  |
| TTCATTCTC   | CTGTTGTAGT | GAAAGGTGCG  | CCCTCTGGAG  | CCTCCCAGGG | TGGGTGTGCA | 840  |
| GGTCACAATG  | ATGAATGTAT | GATCGTGTTC  | CCATTACCCA  | AAGCCTTAA  | ATCCCTCATG | 900  |
| CTCAGTACAC  | CAGGGCAGGT | CTAGCATTTC  | TTCATTAGT   | GTATGCTGTC | CATTGATGCA | 960  |
| ACCACCTCAG  | GACTCCTGGA | TTCTCTGCT   | AGTTGAGCTC  | CTGCATGCTG | CCTCCTTGGG | 1020 |
| GAGGTGAGGG  | AGAGGGCCCA | TGGTTCAATG  | GGATCTGTGC  | AGTTGTAACA | CATTAGGTGC | 1080 |

TTAATAAACAA GAAGCTGTGA TGTTAAAAAA AAAAAAAA

1119

## (2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 164 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asn | Glu | Leu | Phe | Cys | Ser | Gly | Val | Leu | Val | His | Pro | Gln | Trp |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 15  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ser | Ala | Ala | His | Cys | Phe | Gln | Asn | Ser | Tyr | Thr | Ile | Gly | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 30  |
| 20  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Leu | His | Ser | Leu | Glu | Ala | Asp | Gln | Glu | Pro | Gly | Ser | Gln | Met | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 45  |
| 35  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ala | Ser | Leu | Ser | Val | Arg | His | Pro | Glu | Tyr | Asn | Arg | Pro | Leu | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 60  |
| 50  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Asp | Leu | Met | Leu | Ile | Lys | Leu | Asp | Glu | Ser | Val | Ser | Glu | Ser |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 80  |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Thr | Ile | Arg | Ser | Ile | Ser | Ile | Ala | Ser | Gln | Cys | Pro | Thr | Ala | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 95  |
| 85  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Cys | Leu | Val | Ser | Gly | Trp | Gly | Leu | Leu | Ala | Asn | Asp | Ala | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 110 |
| 100 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ala | Ile | Gln | Ser | Xaa | Thr | Val | Gly | Gly | Trp | Glu | Cys | Glu | Lys | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 125 |
| 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gln | Pro | Trp | Gln | Gly | Cys | Thr | Ile | Ser | Ala | Thr | Ser | Ser | Ala | Arg |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 130 |
| 130 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Cys | Cys | Ile | Leu | Thr | Gly | Cys | Ser | Leu | Leu | Leu | Thr | Ala | Ser |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 145 |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

|     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |
|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|-----|
| 150 |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 155 |
|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|-----|

|     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |
|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|-----|
| 155 |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 160 |
|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|-----|

|     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |
|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|--|--|--|
| Pro | Gly | Thr | Leu |  |  |  |  |  |  |  |  |  |  |  |  |
|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|--|--|--|

## (2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCC TTGGTGTTC AAGCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT

60

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| CCAGCTGCC  | CCGGCGGGG  | GATGCGAGGC | TCGGAGCACC | CTTGGCCGGC | TGTGATTGCT  | 120 |
| GCCAGGGACT | GTTCATCTCA | GCTTTCTGT  | CCCTTGCTC  | CCGGCAAGCG | CTTCTGCTGA  | 180 |
| AAGTTCATAT | CTGGAGCCTG | ATGTCTAAC  | GAATAAAGGT | CCCATGCTCC | ACCCGAAAAAA | 240 |
| AAAAAAAAAA |            |            |            |            |             | 250 |

## (2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

|                          |             |            |            |            |            |     |
|--------------------------|-------------|------------|------------|------------|------------|-----|
| ACTAGTCCAG               | TGTGGTGGAA  | TTCCATTGTG | TTGGGCCCAA | CACAATGGCT | ACCTTTAAC  | 60  |
| TCACCCAGAC               | CCCCCCCCCTG | CCCGTGGCCC | ACGCTGCTGC | TAACGACAGT | ATGATGCTTA | 120 |
| CTCTGCTACT               | CGGAAACTAT  | TTTATGTAA  | TTAATGTATG | CTTTCTTGT  | TATAAATGCC | 180 |
| TGATTTAAAA AAAAAAAAAA AA |             |            |            |            |            | 202 |

## (2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

|                        |            |            |             |            |            |     |
|------------------------|------------|------------|-------------|------------|------------|-----|
| TCCYTTGKT              | NAGGTTKKG  | AGACAMCCCK | AGACCTWAAN  | CTGTGTCACA | GACTTCYNGG | 60  |
| AATGTTAGG              | CAGTGTAGT  | AATTCYTG   | TAATGATTCT  | GTTATTACTT | TCCTNATTCT | 120 |
| TTATTCTCT              | TTCTCTGAA  | GATTAATGAA | GTTGAAAATT  | GAGGTGGATA | AATACAAAAA | 180 |
| GGTAGTGTGA             | TAGTATAAGT | ATCTAAGTGC | AGATGAAAGT  | GTGTTATATA | TATCCATTCA | 240 |
| AAATTATGCA             | AGTTAGTAAT | TACTCAGGGT | TAACTAAATT  | ACTTTAATAT | GCTGTTGAAC | 300 |
| CTACTCTGTT             | CCTTGGCTAG | AAAAAATTAT | AAACAGGACT  | TTGTTAGTT  | GGGAAGCCAA | 360 |
| ATTGATAATA             | TTCTATGTTC | AAAAAGTTGG | GCTATACATA  | AATTATTAAG | AAATATGGAW | 420 |
| TTTTATTCCC             | AGGAATATGG | KGTICATTIT | ATGAATAATTA | CSCRGGATAG | AWGTWTGAGT | 480 |
| AAAAYCAGTT             | TTGGTWAATA | YGTWAATATG | TCMTAAATAA  | ACAAKGCTT  | GACTTATTTC | 540 |
| CAAAAAAAAAA AAAAAAAAAA |            |            |             |            |            | 558 |

## (2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ACAGGGWTK  | GRGGATGCTA | AGSCCCCRGA | RWTYGTTGA  | TCCAACCTG  | GCTTWTTTTC | 60  |
| AGAGGGAAA  | ATGGGGCCTA | GAAGTTACAG | MSCATYTAGY | TGGTGCGMTG | GCACCCCTGG | 120 |
| CSTCACACAG | ASTCCCCAGT | AGCTGGGACT | ACAGGCACAC | AGTCACTGAA | GCAGGCCCTG | 180 |
| TTWGCAATT  | ACGTTGCCAC | CTCCAACTTA | AACATTCTTC | ATATGTGATG | TCCTTAGTCA | 240 |
| CTAAGGTTAA | ACTTTCCCAC | CCAGAAAAGG | CAACTTAGAT | AAAATCTTAG | AGTACTTTCA | 300 |
| TACTMTTCTA | AGTCCTCTTC | CAGCTCACT  | KKGAGTCCTM | CYTGGGGTT  | GATAGGAANT | 360 |
| NTCTCTTGGC | TTTCTCAATA | AARTCTCTAT | YCATCTCATG | TTTAATTGG  | TACGCATARA | 420 |

AWTGSTGARA AAATTAAAAAT GTTCTGGTTY MACTTAAAAA ARAAAAAAAA AAAAAAAA 479

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

|                        |                                             |     |
|------------------------|---------------------------------------------|-----|
| AGGCGGGAGC AGAACGCTAAA | GCCAAAGCCC AAGAACAGTG GCAGTGCCAG CACTGGTGCC | 60  |
| AGTACCAAGTA CCAATAACAG | TGCCAGTGCC AGTGCAGCA CCAGTGGTGG CTTCACTGCT  | 120 |
| GGTGCCAGCC TGACCGCCAC  | TCTCACATTG GGGCTCTCG CTGGCCCTGG TGGAGCTGGT  | 180 |
| GCCAGCAACCA GTGGCAGCTC | TGGTGCCGTG GGTTTCTCCT ACAAGTGAGA TTTTAGATAT | 240 |
| TGTTAACCTCT GCAAGTCCTT | CTCTTCAAGC CAGGGTGCAT CCTCAGAAAC CTACTCAACA | 300 |
| CAGCACTCTA GGCAGCCACT  | ATCAATCAAT TGAAGTTGAC ACTCTGCATT ARATCTATT  | 360 |
| GCCATTTCAA AAAAAAAA    | AAAAA 384                                   | 384 |

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

|                                                                   |               |
|-------------------------------------------------------------------|---------------|
| ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTYNT CCRGTATKAC             | CTCAACGAGC 60 |
| AGGGAGATCG AGTCTATACG CTGAAGAAAT TTGACCCGAT GGGACAACAG ACCTGCTCAG | 120           |
| CCCATCCTGC TCGGTTCTCC CCAGATGACA AATACTCTSG ACACCGAATC ACCATCAAGA | 180           |
| AACGCTTCAA GGTGCTCATG ACCCAGCAAC CGCGCCCTGT CCTCTGAGGG TCCCTTAAAC | 240           |
| TGATGCTTT TCTGCCACCT GTTACCCCTC GGAGACTCCG TAACCAAACCT CTTGGACTG  | 300           |
| TGAGCCCTGA TGCCCTTTTG CCAGCCATAC TCTTGGCAT CCAGTCTCTC GTGGCGATTG  | 360           |
| ATTATGTTG TGTGAGGCAA TCATGGTGC ATCACCCATA AAGGGAACAC ATTTGACTTT   | 420           |
| TTTTCTCAT ATTAAATT ACTACMAGAW TATTWMAGAW WAAATGAWTT GAAAAACTST    | 480           |
| AAAAAAAAA AAAA 496                                                | 496           |

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GCTGGTAGCC TATGGCGKGG CCCACGGAGG GGCTCCTGAG GCCACGGRAC AGTGACTTCC | 60  |
| CAAGTATCYT GCGCSGCGTC TTCTACCGTC CCTACCTGCA GATCTTCGGG CAGATTCCCC | 120 |
| AGGAGGACAT GGACGTGGCC CTCATGGAGC ACAGCAAATG YTCTGCGGAG CCCGGCTTCT | 180 |
| GGGCACACCC TCCTGGGGCC CAGGCGGGCA CCTGCGTCTC CCAGTATGCC AACTGGCTGG | 240 |
| TGGTGCTGCT CCTCGTCATC TTCTGCTCG TGGCCAAAT CCTGCTGGTC AACTTGCTCA   | 300 |
| TTGCCATGTT CAGTTACACA TTCGGCAAAG TACAGGGCAA CAGCGATCTC TACTGGGAAG | 360 |
| GCGCAGCGTT ACCGCGCTCAT CGGG                                       | 384 |

## (2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GAGTTAGCTC CTCCACAACC TTGATGAGGT CGTCTGCAGT GGCCTCTCGC TTCATACCGC  | 60  |
| TNCCATCGTC ATACTGTAGG TTTGCCACCA CYTCCTGGCA TCTTGGGGCG GCNTAATATT  | 120 |
| CCAGGAAACT CTCATCAAG TCACCGTCGA TGAAACCTGT GGGCTGGTTC TGTCTTCCGC   | 180 |
| TCGGTGTGAA AGGATCTCCC AGAAGGAGTG CTCGATCTTC CCCACACTTT TGATGACTTT  | 240 |
| ATTGAGTCGA TTCTGCATGT CCAGCAGGAG GTTGTACCAAG CTCTCTGACA GTGAGGTCAC | 300 |
| CAGCCCTATC ATGCCCTTGA MCGTCCGAA GARCACCGAG CCTTGTGTGG GGGKKGAAGT   | 360 |
| CTCACCCAGA TTCTGCATTA CCAGAGAGCC GTGCAAAG ACATTGACAA ACTCGCCAG     | 420 |
| GTGAAAAAAAG AMCAMCTCT GGARGTGCTN GCCGCTCTC GTCMGTGTTGGT GGCAGCCGTW | 480 |
| TCCTTTTGAC ACACAAACAA GTTAAAGGCA TTTTCAGCCCC CCAGAAANTT GTCATCATCC | 540 |
| AAGATNTCGC ACAGCACTNA TCCAGTTGGG ATTAAAT                           | 577 |

## (2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| AACATCTTCC TGTATAATGC TGTGTAATAT CGATCCGATN TTGTCGSGTG AGAATYCATW  | 60  |
| ACTKGAAAAA GMAACATTAA AGCCTGGACA CTGGTATTAA AATTACAAT ATGCAACACT   | 120 |
| TTAACACAGTG TGTCAATCTG CTCCCYNAC TTTGTCATCA CCAGTCTGGG AAKAAGGGTA  | 180 |
| TGCCCTATTAC ACACCTGTTA AAAGGGCGCT AAGCATTTTT GATTCAACAT CTTTTTTTTT | 240 |
| GACACAAGTC CGAAAAAAAGC AAAAGTAAAC AGTTATYAT TTGTTAGCCA ATTCACTTTC  | 300 |
| TTCATGGGAC AGAGCCATYT GATTTAAAAA GCAAATTGCA TAATATTGAG CTTYGGGAGC  | 360 |
| TGATATTGAG GCGGAAGAGT AGCCTTCTA CTTCAACAGA CACAACCTCCC TTTCATATTG  | 420 |
| GGATGTTNAC NAAAGTWATG TCTCTWACAG ATGGGATGCT TTTGTGGCAA TTCTGTTCTG  | 480 |
| AGGATCTCCC AGTTTATTAA CCACCTGCAC AAGAAGGCGT TTTCTCCTC AGGC         | 534 |

## (2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGAAACCAGT ATCTCTAAA ACAACCTCTC ATACCTTG TG GACCTAATT TGTGTGCGTG  | 60  |
| TGTGTGTGCG CGCATATTAT ATAGACAGGC ACATCTTTT TACTTTTGTA AAAGCTTATG  | 120 |
| CCTCTTGGT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT  | 180 |
| TTGTCTTCTG TGTAAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT | 240 |
| TTTATTGAC ATGAAGGAAA TTTCCAGATN ACAACACTNA CAAACTCTCC CTKGACKARG  | 300 |
| GGGGACAAAG AAAAGCAAAA CTGAMCATAA RAAACAATWA CCTGGTGAGA ARTTGCATAA | 360 |
| ACAGAAATWR GGTAGTATAT TGAARNACAG CATCATTAAA RMGTTWTKTT WTTCTCCCTT | 420 |

|                       |             |            |             |            |            |     |
|-----------------------|-------------|------------|-------------|------------|------------|-----|
| GCAAAAAACA TGTACNGACT | TCCC GTTGAG | TAATGCCAAG | TTGTTTTTTT  | TATNATAAAA | 480        |     |
| CTTGCCCTTC            | ATTACATGTT  | TNAAAGTGGT | GTGGTGGGCC  | AAAATATTGA | AATGATGGAA | 540 |
| CTGACTGATA            | AAGCTGTACA  | AATAAGCAGT | GTGCCTAACCA | AGCAACACAG | TAATGTTGAC | 600 |
| ATGCTTAATT            | CACAAATGCT  | AATTCATTA  | AAAATGTTG   | CTAAAATACA | CTTTGAAC   | 660 |
| TTTTCTGTN             | TTCCCAGAGC  | TGAGATNTA  | GATTTATGT   | AGTATNAAGT | GAAAAANTAC | 720 |
| GAAAATAATA            | ACATTGAAGA  | AAAANANAAA | AAANAAAAAA  | A          |            | 761 |

## (2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

|             |             |            |            |             |            |     |
|-------------|-------------|------------|------------|-------------|------------|-----|
| TTTTTTTTTT  | TTTGCCTGATN | CTACTATTTT | ATTCAGGAG  | GTGGGGGTGT  | ATGCACCGCA | 60  |
| CACCGGGGCT  | ATNAGAAGCA  | AGAAGGAAGG | AGGGAGGGCA | CAGCCCCCTTG | CTGAGCAACA | 120 |
| AAGCCGCCCTG | CTGCCTTCTC  | TGTCTGTCTC | CTGGTGCAGG | CACATGGGG   | GACCTTCCCC | 180 |
| AAGGCAGGGG  | CCACCACTCC  | AGGGGTGGGA | ATACAGGGGG | TGGGANGTGT  | GCATAAGAAG | 240 |
| TGATAGGCAC  | AGGCCACCCC  | GTACAGACCC | CTCGGCTCT  | GACAGGTNGA  | TTTCGACCA  | 300 |
| GTCATTGTGC  | CCTGCCAGG   | CACAGCGTAN | ATCTGGAAA  | GACAGAATGC  | TTTCCTTTTC | 360 |
| AAATTGGCT   | NGTCATNGAA  | NGGGCANTTT | TCCAANTTNG | GCTNGGTCTT  | GGTACNCTTG | 420 |
| GTTGGGCCCA  | GTCCTNCGTC  | CAAAAANTAT | TCACCCNNCT | CCNAATTGCT  | TGCNGGNCCC | 480 |
|             |             |            |            |             |            | 482 |

## (2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTAAAACA | GTTTTCAC   | ACAAAATT   | TTAGAAGAAT | AGTGGTTTTG | 60  |
| AAAACCTCTG | CATCCAGTGA | GAAC       | TACCAT     | ACACCACATT | ACAGCTNGGA | 120 |
| AATGTCTGGT | CAAATGATAC | AATGG      | AAACCA     | TTCAATCTTA | CACATGCACG | 180 |
| CGCTTTGAC  | ATACAATGCA | CAAA       | AAAAAA     | AGGGGGGGGG | GACCACATGG | 240 |
| TAAGTACTCA | TCAACATAC  | TAAGACACAG | TTCTAGTCCA | GTCNAAAATC | AGAACTGCNT | 300 |
| TGA        | AAAATTT    | CATGTATGCA | ATCCAACAA  | AGAACTTNAT | TGGTGATCAT | 360 |
| CTACATCNAC | CTTGATCATT | GCCAGGAACN | AAAAGTTNAA | ANCACNCNGT | ACAAAANAA  | 420 |
| TCTGTAATTN | ANTTCACCT  | CCGTACNGAA | AAATNTNNNT | TATACACTCC | C          | 471 |

## (2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GAGGGATTGA | AGGTCTGTT  | TASTGTCGGM | CTGTTCA    | ACCAACTCTA | ACAAGTTGCT | 60  |
| GTCTTCCACT | CACTGTCTGT | AAGCTTTA   | ACCCAGACWG | TATCTTCATA | AATAGAACAA | 120 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ATTCTTCACC | AGTCACATCT | TCTAGGACCT | TTTGGATTC  | AGTTAGTATA | AGCTCTCCA  | 180 |
| CTTCCTTGT  | TAAGACTTCA | TCTGGAAAG  | TCTTAGTTT  | TGTAGAAAGG | AATTYAATTG | 240 |
| CTCGTTCTCT | AACAATGTCC | TCTCCTTGAA | GTATTTGGCT | GAACAACCCA | CCTAAAGTCC | 300 |
| CTTTGTGCAT | CCATTTAAA  | TATACTTAAT | AGGGCATTGK | TNCACTAGGT | TAAATTCTGC | 360 |
| AAGAGTCATC | TGTCTGCAA  | AGTTGCGTTA | GTATATCTGC | CA         |            | 402 |

## (2) INFORMATION FOR SEQ ID NO:192:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

|            |             |             |            |             |             |     |
|------------|-------------|-------------|------------|-------------|-------------|-----|
| GAGCTCGGAT | CCAATAATCT  | TTGTCTGAGG  | GCAGCACACA | TATNCAGTGC  | CATGGNAACT  | 60  |
| GGTCTACCCC | ACATGGGAGC  | AGCATGCCGT  | AGNTATATAA | GGTCATTCCC  | TGAGTCAGAC  | 120 |
| ATGCYTYTTT | GAYTACCGTG  | TGCCAAGTGC  | TGGTGATTCT | YAACACACYT  | CCATCCCGYT  | 180 |
| CTTTGTGGA  | AAAAGCTGGCA | CTTKTCTGGA  | ACTAGCARGA | CATCACTTAC  | AAATTACACC  | 240 |
| ACGAGACACT | TGAAAGGTGT  | AAACAAAGCGA | YTCTTGATT  | GCTTTTGTC   | CCTCCGGCAC  | 300 |
| CAGTTGTCAA | TACTAACCCG  | CTGGTTTGCC  | TCCATCACAT | TTGTGATCTG  | TAGCTCTGGA  | 360 |
| TACATCTCCT | GACAGTACTG  | AAGAACTTCT  | TCTTTGTTT  | CAAAGCARC   | TCTTGGTGCC  | 420 |
| TGTTGGATCA | GGTTCCCAATT | TCCCAGTCYG  | AATGTTCACA | TGGCATATT   | WACTTCCCAC  | 480 |
| AAAACATTGC | GATTTGAGGC  | TCAGCAACAG  | CAAATCCTGT | TCCGGCATTG  | GCTGCAAGAG  | 540 |
| CCTCGATGTA | GCCGGCCAGC  | GCCAAGGCAG  | GCGCCGTGAG | CCCCACCAAGC | ACCAGAAAGCA | 600 |
| G          |             |             |            |             |             | 601 |

## (2) INFORMATION FOR SEQ ID NO:193:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

|            |            |            |             |             |             |     |
|------------|------------|------------|-------------|-------------|-------------|-----|
| ATACAGGCCA | NATCCCACCA | CGAAGATGCG | CTTGGTGA    | GAGAACCTGA  | TGCGGTCACT  | 60  |
| GGTCCCCTG  | TAGCCCCAGC | GACTCTCCAC | CTGCTGGAAAG | CGGTTGATGC  | TGCACTCYTT  | 120 |
| CCCAACGCAG | GCAGMAGCGG | GSCCGGTCAA | TGAACCTCCAY | TCGTGGCTTG  | GGGTKGACGG  | 180 |
| TKAAGTGCAG | GAAGAGGCTG | ACCACCTCGC | GGTCCACCAAG | GATGCCCGAC  | TGTGCGGGAC  | 240 |
| CTGCAGCGAA | ACTCCTCGAT | GGTCATGAGC | GGGAAGCGAA  | TGAGGCCCCAG | GGCCTTGGCCC | 300 |
| AGAACCTTCC | GCCTGTTCTC | TGGCGTCACC | TGCACTGCT   | GCCGCTGACA  | CTCGGCCTCG  | 360 |
| GACCAGCGGA | AAACAGGCR  | TGAACAGCGC | CACCTCACGG  | ATGCCCACTG  | TGTCGCGCTC  | 420 |
| CAGGAMMGS  | ACCAGCGTGT | CCAGGTCAAT | GTGGTGAAG   | CCCTCCGCGG  | GTRATGGCGT  | 480 |
| CTGCAGTGT  | TTTGTGATG  | TTCTCCAGGC | ACAGGCTGGC  | CAGCTGCGGT  | TCATCGAAGA  | 540 |
| GTCGCGCTG  | CGTGAGCAGC | ATGAAGGCGT | TGTCGGCTCG  | CAGTTCTTCT  | TCAGGAACTC  | 600 |
| CACGCAAT   |            |            |             |             |             | 608 |

## (2) INFORMATION FOR SEQ ID NO:194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| GAACGGCTGG | ACCTTGCCTC | GCATTGTGCT | TGCTGGCAGG | GAATACCTTG  | GCAAGCAGYT | 60  |
| CCAGTCCGAG | CAGCCCCAGA | CCGCTGCCGC | CCGAAGCTAA | GCCTGCCTCT  | GGCCTTCCCC | 120 |
| TCCGGCTCAA | TGCAGAACCA | GTAGTGGGAG | CACTGTGTTT | AGAGTTAACG  | GTGAACACTG | 180 |
| TTTGATTTTA | CTTGGGAATT | TCCTCTGTTA | TATAGCTTTT | CCCAATGCTA  | ATTTCCAAC  | 240 |
| AACAACAACA | AAATAACATG | TTTGCCTGTT | AAGTTGTATA | AAAGTAGGGTG | ATTCTGTATT | 300 |
| TAAAGAAAAT | ATTACTGTAA | CATAACTGC  | TTGCAATTTC | TGTATTTATT  | GKTNCTSTGG | 360 |
| AAATAAATAT | AGTTATTAAA | GGTTGTCANT | CC         |             |            | 392 |

## (2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

|            |            |             |            |             |            |     |
|------------|------------|-------------|------------|-------------|------------|-----|
| CCSTTKGAGG | GGTKAGGKYC | CAGTTYCCGA  | GTGGAAGAAA | CAGGCCAGGA  | GAAGTGCCTG | 60  |
| CCGAGCTGAG | GCAGATGTT  | CCACAGTGAC  | CCCCAGAGCC | STGGGSTATA  | GTYTCTGACC | 120 |
| CCTCNCAAGG | AAAGACCACS | TTCTGGGAC   | ATGGGCTGGA | GGGCAGGACC  | TAGAGGCACC | 180 |
| AAGGAAGGC  | CCCATTCCGG | GGSTGTTCCC  | CGAGGAGGAA | GGGAAGGGC   | TCTGTGTGCC | 240 |
| CCCCASGAGG | AAGAGGCCCT | GAGTCCTGGG  | ATCAGACACC | CCTTCACGTG  | TATCCCCACA | 300 |
| CAAATGCAAG | CTCACCAAGG | TCCCCCTCTCA | GTCCCCCTCC | STACACCCCTG | AMCGGCCACT | 360 |
| GSCSCACACC | CACCCAGAGC | ACGCCACCCG  | CCATGGGGAR | TGTGCTCAAG  | GARTCGCNGG | 420 |
| GCARCGTGG  | CATCTNGTCC | CAGAAGGGGG  | CAGAATCTCC | AATAGANGGA  | CTGARCMSTT | 480 |
| GCTNAAAAAA | AAAAANAAAA | AA          |            |             |            | 502 |

## (2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| GGTTACTTGG | TTTCATTGCC | ACCACTTAGT | GGATGTCATT  | TAGAACCATT | TTGTCTGCTC | 60  |
| CCTCTGGAAC | CCTTGGCGAG | AGCGGACTTT | GTAAATTGTTG | GAGAATAACT | GCTGAATT   | 120 |
| WAGCTGTTK  | GAGTTGATTS | GCACCACTGC | ACCCACAAC   | TCAATATGAA | AACYAWTTGA | 180 |
| ACTWATTAT  | TATCTTGTGA | AAAGTATAAC | AATGAAAATT  | TTGTTCATAC | TGTATTKATC | 240 |
| AAGTATGATG | AAAAGCAAWA | GATATATATT | CTTTTATTAT  | GTAAATTAT  | GATTGCCATT | 300 |
| ATTAATCGGC | AAAATGTGGA | GTGTATGTT  | TTTTCACAGT  | AATATATGCC | TTTTGTAACT | 360 |
| TCACCTGGTT | ATTTATTGTT | AAATGARTTA | CAAAATTCTT  | AATTAAAGAR | AATGGTATGT | 420 |
| WATATTTATT | TCATTAATT  | CTTTCCTKG  | TTACGTWAAT  | TTGAAAAGA  | WTGCATGATT | 480 |
| TCTTGACAGA | AATCGATCTT | GATGCTGTGG | AAAGTAGTTG  | ACCCACATCC | CTATGAGTT  | 540 |
| TTCTTAGAAT | GTATAAAGGT | TGTAGCCAT  | CNAACTTCAA  | AGAAAAAAAT | GACCACATAC | 600 |
| TTTGCATCA  | GGCTGAAATG | TGGCATGCTN | TTCTAATTCC  | AACTTTATAA | ACTAGCAAAN | 660 |
|            |            |            |             |            |            | 665 |

## (2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTNTTTTT | TTTTTTTGC  | AGGAAGGATT | CCATTTATTG | TGGATGCATT | TTCACAATAT | 60  |
| ATGTTTATTG | GAGCGATCCA | TTATCAGTGA | AAAGTATCAA | GTGTTATAA  | NATTTTTAGG | 120 |
| AAGGCAGATT | CACAGAACAT | GCTNGTCNGC | TTGCAGTTT  | ACCTCGTANA | GATNACAGAG | 180 |
| AATTATAGTC | NAACCAGTAA | ACNAGGAATT | TACTTTCAA  | AAGATTAAT  | CCAAACTGAA | 240 |
| CAAAATTCTA | CCCTGAAACT | TACTCCATCC | AAATATTGGA | ATAANAGTCA | GCAGTGATAC | 300 |
| ATTCTCTTCT | GAACTTAGA  | TTTCTAGAA  | AAATATGTA  | TAGTGATCAG | GAAGAGCTCT | 360 |
| TGTTCAAAAG | TACAACNAAG | CAATGTTCCC | TTACCATAGG | CCTTAATTCA | AACTTTGATC | 420 |
| CATTTCACTC | CCATCACGGG | AGTCAATGCT | ACCTGGGACA | CTTGTATTT  | GTTCATNCTG | 480 |
| ANCNTGGCTT | AA         |            |            |            |            | 492 |

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| TTTNTTTGN  | ATTCANTCT  | GTANNAANTA | TTTCATTAT  | TTTTATTANA | AAAATATNAA  | 60  |
| TGNTCCACN  | ACAAATCATN | TTACNTNAGT | AAAGGCCAN  | CTACATTGTA | CAACATACAC  | 120 |
| TGAGTATATT | TTGAAAAGGA | CAAGTTAAA  | GTANACNCAT | ATTGCCGANC | ATANCACATT  | 180 |
| TATACATGGC | TTGATTGATA | TTTAGCACAG | CANAAAATG  | GTGAGTTACC | AGAAAANAAAT | 240 |
| NATATATGTC | AATCNGATT  | AAGATACAAA | ACAGATCCTA | TGGTACATAN | CATCNGTAG   | 300 |
| GAGTTGTGGC | TTTATGTTA  | CTGAAAGTCA | ATGCAGTTCC | TGTACAAAGA | GATGGCCGTA  | 360 |
| AGCATTCTAG | TACCTCTACT | CCATGGTTAA | GAATCGTACA | CTTATGTTA  | CATATGTNCA  | 420 |
| GGGTAAGAAT | TGTGTTAAGT | NAANTTATGG | AGAGGTCCAN | GAGAAAATT  | TGATNCAA    | 478 |

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| AGTGACTTGT | CCTCCAACAA | AACCCCTTGA  | TCAAGTTGT  | GGCACTGACA | ATCAGACCTA | 60  |
| TGCTAGTTCC | TGTCATCTAT | TCGCTACTAA  | ATGCAGACTG | GAGGGGACCA | AAAAGGGGCA | 120 |
| TCAACTCCAG | CTGGATTATT | TTGGAGCCTG  | CAAATCTATT | CCTACTTGT  | CGGACTTTGA | 180 |
| AGTGATTCAG | TTTCCTCTAC | GGATGAGAGA  | CTGGCTCAAG | AATATCCTCA | TGCAGCTTTA | 240 |
| TGAAGCCNAC | TCTGAACACG | CTGGTTATCT  | NAGATGAGAA | NCAGAGAAAT | AAAGTCNAGA | 300 |
| AAATTTACCT | GGANGAAAAG | AGGCTTNGG   | CTGGGGACCA | TCCCATTGAA | CCTTCTCTTA | 360 |
| ANGGACTTTA | AGAANAAAAT | ACACATGTA   | TGTGTTATCC | TGGTGCCNNG | CCGTTTANTG | 420 |
| AACNTNGACN | NCACCCTTNT | GGAAATANANT | CTTGACNGCN | TCCTGAACTT | GCTCCTCTGC | 480 |
| GA         |            |             |            |            |            | 482 |

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| CGGCCGCAAG | TGCACTCCA  | GCTGGGGCCG  | TGCGGACGAA | GATTCTGCCA | GCAGTTGGTC | 60  |
| CGACTGCGAC | GACGGCGCG  | GCGACAGTCG  | CAGGTGCAGC | GCGGGCGCCT | GGGGTCTTGC | 120 |
| AAGGCTGAGC | TGACGCCGA  | GAGGTCTGTGT | CACGTCCCAC | GACCTTGACG | CCGTCGGGGA | 180 |
| CAGCCGGAAC | AGAGCCGGT  | GAANGCGGGA  | GGCCTCGGGG | AGCCCCTCGG | GAAGGGCGGC | 240 |
| CCGAGAGATA | CGCAGGTGCA | GGTGGCCGCC  |            |            |            | 270 |

## (2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| TTTTTTTTT  | TTTTGGAATC | TACTGCGAGC | ACAGCAGGTC | AGCAACAAAGT | TTATTTGCA  | 60  |
| GCTAGCAAGG | TAACAGGGTA | GGGCATGGTT | ACATGTTCA  | GTCAACTTCC  | TTTGTCTGG  | 120 |
| TTGATTGGTT | TGTCTTTATG | GGGGCGGGGT | GGGGTAGGGG | AAANCGAAC   | ANAANTAAC  | 180 |
| TGGAGTGGGT | GCACCCTCCC | TGTAGAACCT | GGTACNAAA  | GCTTGGGCA   | GTTCACCTGG | 240 |
| TCTGTGACCG | TCATTTCTT  | GACATCAATG | TTATTAGAAG | TCAGGATATC  | TTTTAGAGAG | 300 |
| TCCACTGTNT | CTGGAGGGAG | ATTAGGGTT  | CTTGCCAANA | TCCAANAAA   | ATCCACNTGA | 360 |
| AAAAGTTGGA | TGATNCANGT | ACNGAATACC | GANGGCATAN | TTCTCATANT  | CGGTGGCCA  | 419 |

## (2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| TTTNNTTTTTT | TTTTTTTTTT  | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT  | 60  |
| TGGCACTTAA  | TCCATTITTA  | TTTCAAATG  | TCTACAAANT | TTNAATNCNC | CATTATACNG  | 120 |
| GTNATTNTNC  | AAAATCTAAA  | NNTTATCAA  | ATNTNAGCCA | AANTCCTTAC | NCAAATNNAA  | 180 |
| TACNCNCAAA  | AATCAAAAT   | ATACNTNTCT | TTCAGCAAAC | TTNGTTACAT | AAATTAAAAAA | 240 |
| AATATATACG  | GCTGGTGT    | TCAAAGTACA | ATTATCTAA  | CACTGCAAAC | ATNTTNNAA   | 300 |
| GGAACATAAAA | TAAAAAAAAAA | CACTNCCGA  | AAGGTTAAAG | GGAACAACAA | ATTCTNTTAA  | 360 |
| CAACANCNNC  | NATTATAAAA  | ATCATATCTC | AAATCTTAGG | GGAATATATA | CTTCACACNG  | 420 |
| GGATCTTAAAC | TTTACTNCA   | CTTTGTTAT  | TTTTTANAA  | CCATTGTNTT | GGGCCAACAA  | 480 |
| CAATGGNAAT  | NCCNCCNCCN  | TGGACTAGT  |            |            |             | 509 |

## (2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

|            |              |            |            |             |             |     |
|------------|--------------|------------|------------|-------------|-------------|-----|
| TTTTTTTTTT | TTTTTTTGAGCC | CCCCCTCTT  | ATAAAAACA  | AGTTACCATT  | TTATTTACT   | 60  |
| TACACATATT | TATTTTATAA   | TTGGTATTAG | ATATTCAAAA | GGCAGCTTTT  | AAAATCAAAC  | 120 |
| TAATGGAAA  | CTGCCTTAGA   | TACATAATTC | TTAGGAATTA | GCTTAAATC   | TGCCCTAAAGT | 180 |
| GAAAATCTTC | TCTAGCTCTT   | TTGACTGTAA | ATTTTGACT  | CTTGAAAC    | ATCCAAATTC  | 240 |
| ATTTTCTTG  | TCTTTAAAT    | TATCTAATCT | TTCCATTTTT | TCCCTATTCC  | AAGTCAATT   | 300 |
| GCTTCTCTAG | CCTCATTTCC   | TAGCTCTTAT | CTACTATTAG | TAAGTGGCTT  | TTTCTCTAAA  | 360 |
| AGGGAAAACA | GGAAGAGANA   | ATGGCACACA | AAACAAACAT | TTTATAATTCA | TATTTCTACC  | 420 |
| TACGTTAATA | AAATAGCATT   | TTGTGAAGCC | AGCTCAAAG  | AAGGCTTAGA  | TCCTTTATG   | 480 |
| TCCATTITAG | TCACTAAACG   | ATATCNAAG  | TGCCAGAATG | CAAAGGTTT   | GTGAACATTT  | 540 |
| ATTCAAAAGC | TAATATAAGA   | TATTCACAT  | ACTCATCTT  | CTG         |             | 583 |

## (2) INFORMATION FOR SEQ ID NO:204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

|             |             |            |             |             |             |     |
|-------------|-------------|------------|-------------|-------------|-------------|-----|
| TTTTTTTTNT  | TTTTTTTTTT  | TTTTTNCTC  | TTCTTTTTT   | TTGANAATGA  | GGATCGAGTT  | 60  |
| TTTCACCTCTC | TAGATAGGGC  | ATGAAGAAAA | CTCATCTTC   | CAGCTTTAAA  | ATAACAAATCA | 120 |
| AATCTCTTAT  | GCTATATCAT  | ATTTAAGTT  | AAACTAATGA  | GTCACTGGCT  | TATCTCTCC   | 180 |
| TGAAGGAAAT  | CTGTTCATTC  | TTCTCATTC  | TATAGTTATA  | TCAAGTACTA  | CCTTGATAT   | 240 |
| TGAGAGGTTT  | TTCTTCTCTA  | TTTACACATA | TATTTCATG   | TGAATTGTA   | TCAAACCTTT  | 300 |
| ATTTTCATGC  | AAACTAGAAA  | ATAATGTNTT | CTTTGCATA   | AGAGAAGAGA  | ACAATATNAG  | 360 |
| CATTACAAA   | CTGCTCAAAT  | TGTTGTTAA  | GNTTATCCAT  | TATAATTAGT  | TNGGCAGGAG  | 420 |
| CTAATACAAA  | TCACATTAC   | NGACNAGCAA | TAATAAAACT  | GAAGTACCAAG | TTAAATATCC  | 480 |
| AAAATAATTA  | AAGGAACATT  | TTTAGGCTGG | GTATAATTAG  | CTAACACT    | TTACAAGCAT  | 540 |
| TTATTNAGAA  | TGAATTACACA | TGTTATTATT | CCNTAGCCCAC | ACACAATGG   |             | 589 |

## (2) INFORMATION FOR SEQ ID NO:205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| TTTTNTTTT  | TTTTTCAGT   | AATAATCAGA | ACAATATTAA | TTTTTATATT | AAAATTCA   | 60  |
| AGAAAAGTGC | CTTACATTAA  | ATAAAAGTTT | GTTCCTCAA  | GTCAGAG    | GAATTAGATA | 120 |
| TNGTCTTGAA | CACCAATATT  | AATTGAGGA  | AAATACACCA | AAATACATTA | AGTAAATTAT | 180 |
| TTAAGATCAT | AGAGCTTGTAA | AGTAAAAGA  | TAATAATTGA | CCTCAGAAC  | TCTGAGCATT | 240 |
| AAAAATCCAC | TATTAGCAAA  | TAATTAAC   | TGGACTTCTT | GCTTTAATT  | TGTGATGAAT | 300 |
| ATGGGGTGTC | ACTGGTAAAC  | CAACACATTC | TGAAGGATAC | ATTACTTAGT | GATAGATTCT | 360 |
| TATGTACTTT | GCTANATNAC  | GTGGATATGA | GTTGACAAGT | TTCTCTTCT  | TCAATCTTT  | 420 |
| AAGGGGCNGA | NGAAATGAGG  | AAGAAAAGAA | AAGGATTACG | CATACTGTTC | TTTCTATNGG | 480 |
| AAGGATTAGA | TATGTTCTCT  | TTGCCAATAT | TAAGAAAATA | ATAATGTTA  | CTACTAGTGA | 540 |
| AACCC      |             |            |            |            |            | 545 |

## (2) INFORMATION FOR SEQ ID NO:206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTAGTC | AAGTTTCTNA | TTTTTATTAT | AATTAAAGTC | TTGGTCATT  | 60  |
| CATTTATTAG | CTCTGCAACT | TACATATTAA | AATTAAAGAA | ACGTTNTTAG | ACAACTGTNA | 120 |
| CAATTTATAA | ATGTAAGGTG | CCATTATTGA | GTANATATAT | TCCTCCAAGA | GTGGATGTGT | 180 |
| CCCTTCTCCC | ACCAACTAAT | GAANCAGCAA | CATTAGTTA  | ATTTTATTAG | TAGATNATAC | 240 |
| ACTGCTGCAA | ACGCTAATTC | TCTTCTCCAT | CCCCATGTNG | ATATTGTGTA | TATGTGTGAG | 300 |
| TTGGTNAGAA | TGCATCANCA | ATCTNACAAT | CAACAGCAAG | ATGAAGCTAG | GCNTGGCCTT | 360 |
| TCGGTAAAAA | TAGACTGTGT | CTGTCGAAT  | CAAATGATCT | GACCTATCCT | CGGTGGCAAG | 420 |
| AACTCTTCGA | ACCGCTTCCT | CAAAGGCNGC | TGCCACATTT | GTGGCNTCTN | TTGCACTTGT | 480 |
| TTCAAAA    |            |            |            |            |            | 487 |

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 332 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| TGAATTGGCT | AAAAGACTGC | ATTTTANAA  | CTAGCAACTC | TTATTTCTTT | CCTTTAAAAAA | 60  |
| TACATAGCAT | TAAATCCCAA | ATCCTATTAA | AAGACCTGAC | AGCTTGAGAA | GGTCACTACT  | 120 |
| GCATTTATAG | GACCTTCTGG | TGGTTCTGCT | GTACNTTTG  | AANTCTGACA | ATCCTTGANA  | 180 |
| ATCTTGCAT  | GCAGAGGAGG | TAAAAGGTAT | TGGATTTCA  | CAGAGGAANA | ACACAGCGCA  | 240 |
| GAAATGAAGG | GGCCAGGCTT | ACTGAGCTTG | TCCACTGGAG | GGCTCATGGG | TGGGACATGG  | 300 |
| AAAAGAAGGC | AGCCTAGGCC | CTGGGGAGCC | CA         |            |             | 332 |

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 524 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

|            |            |             |             |             |            |     |
|------------|------------|-------------|-------------|-------------|------------|-----|
| AGGGCGTGGT | GCGGAGGGCG | TTACTGTTTT  | GTCTCAGTAA  | CAATAAAATAC | AAAAAGACTG | 60  |
| GTTGTGTTCC | GGCCCCATCC | AACCACGAAG  | TTGATTCTC   | TTGTGTGCAG  | AGTGACTGAT | 120 |
| TTAAAGGAC  | ATGGAGCTTG | TCACAATGTC  | ACAATGTCAC  | AGTGTGAAGG  | GCACACTCAC | 180 |
| TCCCCCGTGA | TTCACATTAA | GCAACCAACA  | ATAGCTCATG  | AGTCCATACT  | TGAAATACT  | 240 |
| TTTGGCAGAA | TACTTNTTGA | AACTTGCAGA  | TGATAACTAA  | GATCCAAGAT  | ATTTCCAAA  | 300 |
| GTAAAATGAA | GTGGGTCATA | ATATTAATTAA | CCTGTTCACCA | TCAGCTTCCA  | TTTACAAGTC | 360 |
| ATGAGCCCAG | ACACTGACAT | CAAACAAAGC  | CCACTTAGAC  | TCCTCACCAC  | CAGTCTGTCC | 420 |
| TGTCATCAGA | CAGGAGGCTG | TCACCTTGAC  | CAAATTCTCA  | CCAGTCAATC  | ATCTATCCAA | 480 |
| AAACCATTAC | CTGATCCACT | TCCGGTAATG  | CACCACTTG   | GTGA        |            | 524 |

(2) INFORMATION FOR SEQ ID NO:209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGGTGAGGAA ATCCAGAGTT GCCATGGAGA AAATTCCAGT GTCAGCATTC TTGCTCCTTG | 60  |
| TGGCCCTCTC CTACACTCTG GCCAGAGATA CCACAGTCAA ACCTGGAGCC AAAAAGGACA | 120 |
| CAAAGGACTC TCGACCCAAA CTGCCCCAGA CCCTCTCCA                        | 159 |

(2) INFORMATION FOR SEQ ID NO:210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ACTCCCTGGC AGACAAAGGC AGAGGGAGAGA GCTCTGTTAG TTCTGTGTTG TTGAAC TGCC | 60  |
| ACTGAATTTC TTTCCACTTG GACTATTACA TGCCANTTGA GGGACTAATG GAAAAACGTA   | 120 |
| TGGGGAGATT TTANCCAATT TANGNTGTA AATGGGGAGA CTGGGGCAGG CGGGAGAGAT    | 180 |
| TTGCAGGGTG NAAATGGGAN GGCTGGTTG TTANATGAAC AGGGACATAG GAGGTAGGCA    | 240 |
| CCAGGATGCT AAATCA                                                   | 256 |

(2) INFORMATION FOR SEQ ID NO:211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACATTGTTT TTGAGATAA AGCATTGAGA GAGCTCTCCT TAACGTGACA CAATGGAAGG   | 60  |
| ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT  | 120 |
| ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTTAAGGAGA | 180 |
| GGGGAGATAAC ATTNGAAAG AGGACTGAAA GAATACTCA AGTNGGAAA CAGAAAAGA    | 240 |
| AAAAAAAGGAG CAAATGAGAA GCCT                                       | 264 |

(2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACCCAAAAAT CCAATGCTGA ATATTTGGCT TCATTATTCC CANATTCTT GATTGTCAA   | 60  |
| GGATTTAATG TTGTCTCAGC TTGGGCACCT CAGTAGGAC CTAAGGATGC CAGCCGGCAG  | 120 |
| GTTTATATAT GCAGCAACAA TATTCAAGCG CGACAACAGG TTATTGAACT TGCCCGCCAG | 180 |
| TTNAATTTC TTCCCATTGA CTTGGGATCC TTATCATCAG CCAGAGAGAT TGAAAATTAA  | 240 |
| CCCTTACNAC TCTTTACTCT CTGGANAGGG CCAGTGGTGG TAGCTATAAG CTTGGCCACA | 300 |
| TTTTTTTTTC CTTTATTCCCT TTGTCAGA                                   | 328 |

## (2) INFORMATION FOR SEQ ID NO:213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACTTATGAGC AGAGCGACAT ATCCNAGTGT AGACTGAATA AAACGTGAATT CTCTCCAGTT | 60  |
| TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT  | 120 |
| CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAAACT TCTTCCTCAT TCCAAGAGTT  | 180 |
| TTCAATATTT GCATGAACCT GCTGATAANC CATGTTAANA AACAAATATC TCTCTNACCT  | 240 |
| TCTCATCGGT                                                         | 250 |

## (2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACCCAGAACAT CAATGCTGAA TATTTGGCTT CATTATTCCC AGATTCTTTG ATTGTCAAAG | 60  |
| GATTAAATGT TGTCTCAGCT TGGGCACCTC AGTTAGGACC TAAGGTGCC AGCCGGCAGG   | 120 |
| TTTATATATG CAGCAACAAAT ATTCAAGCGC GACAACAGGT TATTGAACTT GCCCGCCAGT | 180 |
| TGAATTTCAT TCCCATTGAC TTGGGATCCT TATCATCAGC CANAGAGATT GAAAATTAC   | 240 |
| CCCTACGACT CTTTACTCTC TGGAGAGGGC CAGTGGTGGT AGCTATAAGC TTGGCCACAT  | 300 |
| TTTTTTTCTC TTATTCCTT TGTCAAGAGT GCGATTCACTC CATATGCTAN AAACCAACAG  | 360 |
| AGTGAACCTT ACAAAATTCC TATAGANATT GTGAATAAAA CCTTACCTAT AGTTGCCATT  | 420 |
| ACTTGCTCT CCCTAATATA CCTC                                          | 444 |

## (2) INFORMATION FOR SEQ ID NO:215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ACTTATGAGC AGAGCGACAT ATCCAAGTGT ANACTGAATA AAACGTGAATT CTCTCCAGTT | 60  |
| TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT  | 120 |

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAAACT TCTTCCTCAT TCCAAGAGTT | 180 |
| TTCATATTT GCATGAACCT GCTGATAAGC CATGTTGAGA AACAAATATC TCTCTGACCT  | 240 |
| TCTCATCGGT AAGCAGAGGC TGTAGGCAC ATGGACCATA GCGAANAAAA AACTTAGTAA  | 300 |
| TCCAAGCTGT TTTCTACACT GTAACCAGGT TTCCAACCAA GGTGGAAATC TCCTATACTT | 360 |
| GGTGCC                                                            | 366 |

## (2) INFORMATION FOR SEQ ID NO:216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CTGTATAAAC AGAACTCCAC TGCANGAGGG AGGGCCGGGC CAGGAGAATC TCCGCTTGTC | 60  |
| CAAGACAGGG GCCTAAGGAG GGTCTCCACA CTGCTNNTAA GGGCTNTTNC ATTTTTTAT  | 120 |
| TAATAAAAAG TNNAAAAGGC CTCTTCTCAA CTTTTTCCC TTNGGCTGGA AAATTTAAA   | 180 |
| ATCAAAAATT TCCTNAAGTT NTCAAGCTAT CATATATACT NTATCCTGAA AAAGCAACAT | 240 |
| AATTCTTCCT TCCCTCCTTT                                             | 260 |

## (2) INFORMATION FOR SEQ ID NO:217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACCTACGTGG GTAAGTTTAN AAATGTTATA ATTTCAGGAA NAGGAACGCA TATAATTGTA | 60  |
| TCTTGCTAT AATTTTCTAT TTTAATAAGG AAATAGAAA TTGGGGTGGG GGGAAATGTAG  | 120 |
| GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACACCACT GAAAAATT   | 180 |
| ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATT AAATTTAGCC ACTTACCTA   | 240 |
| ATATCCTTCA TGCTTGAAA GT                                           | 262 |

## (2) INFORMATION FOR SEQ ID NO:218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCCAA CCCCTGAGCA | 60  |
| CCCCATCAA CTCCCTTTTG TAGTAAACTT GGAACCTTGG AAATGACCAG GCCAAGACTC  | 120 |
| AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGTNTNA NGTCCAGGGT TGCTAGGAAA | 180 |
| ANAAATCAGC AGACACAGGT GTAAA                                       | 205 |

## (2) INFORMATION FOR SEQ ID NO:219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TACTGTTTG TCTCAGTAAC AATAAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA | 60  |
| ACCACGAAGT TGATTCTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA      | 114 |

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| ACTAGCCAGC ACAAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTAC ATTTCTTTA | 60 |
| AAATAAGCAT TTAGTGCTCA GTCCCTACTG AGT                            | 93 |

## (2) INFORMATION FOR SEQ ID NO:221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTANGTGCA GGTGCGCACA AATATTTGTC GATATTCCCT TCATCTTGGG TTCCATGAGG | 60  |
| TCTTTGCCC AGCCTGTGGC TCTACTGTAG TAAGTTCTG CTGATGAGGA GCCAGNATGC   | 120 |
| CCCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCAA CCTCTGT                | 167 |

## (2) INFORMATION FOR SEQ ID NO:222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCCCC | 60  |
| GTTCTTCACC TGTCCCCCAA TCCTTAAAAG GCCATACTGC ATAAAGTCAA CAACAGATAAA | 120 |
| ATGTTTGCTG AATTAAGGAA TGGATGAAAA AAATTAATAA TGAATTTTG CATAATCCAA   | 180 |
| TTTTCTCTTT TATATTCTCA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGGATCTTT   | 240 |
| TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCTTTACA TATATCTGGC ATATTTGAGT   | 300 |

CTCGTATCAA AACAAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T 351

## (2) INFORMATION FOR SEQ ID NO:223

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAAACAAACA AACAAAAAAA ACAATTCTTC ATTCAAGAAA ATTATCTTAG GGACTGATAT | 60  |
| TGGTAATTAT GGTCAATTAA ATWRTRTTK GTGGCATTTTC CTTACATTGT CTTGACAAGA | 120 |
| TTAAAATGTC TGTGCCAAAA TTTTGATTTT TATTTGGAGA CTTCTTATCA AAAGTAATGC | 180 |
| TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTGGAG TGTGCTATT   | 240 |
| TAAAAGATTT TGATTCCCTG GAATGACAAT TATATTTAA CTTTGGTGGG GGAAANAGTT  | 300 |
| ATAGGACAC AGTCTCACT TCTGATACTT GTAAATTAAT CTTTATTGC ACTTGTGTTG    | 360 |
| ACCATTAAGC TATATGTTA AAA                                          | 383 |

## (2) INFORMATION FOR SEQ ID NO:224

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| CCCCCTGAAGG CTTCTTGTAA GAAAATAGTA CAGTTACAAC CAATAGGAAC AACAAAAAGA | 60  |
| AAAAGTTTGT GACATTGTAG TAGGGAGTGT GTACCCCTTA CTCCCCATCA AAAAAAAAAT  | 120 |
| GGATACATGG TTAAAGGATA RAAGGGCAAT ATTTTATCAT ATGTTCTAAA AGAGAAGGAA  | 180 |
| GAGAAAATAC TACTTCTCR AAATGGAAGC CCTTAAAGGT GCTTGATAC TGAAGGACAC    | 240 |
| AAATGTGGCC GTCCATCCTC CTTTARAGTT GCATGACTTG GACACGGTAA CTGTTGCAGT  | 300 |
| TTTARACTCM GCATTGTGAC                                              | 320 |

## CLAIMS

1. A polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.
2. A DNA molecule comprising a nucleotide sequence encoding the polypeptide of claim 1.
3. A DNA molecule having a sequence provided in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224.
4. An expression vector comprising the DNA molecule of claims 2 or 3.
5. A host cell transformed with the expression vector of claim 4.
6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cell lines.
7. A pharmaceutical composition comprising the polypeptide of claim 1 and a physiologically acceptable carrier.
8. A vaccine comprising the polypeptide of claim 1 and a non-specific immune response enhancer.

9. The vaccine of claim 8 wherein the non-specific immune response enhancer is an adjuvant.

10. A vaccine comprising the DNA molecule of claims 2 or 3 and a non-specific immune response enhancer.

11. The vaccine of claim 10 wherein the non-specific immune response enhancer is an adjuvant.

12. A pharmaceutical composition for the treatment of prostate cancer comprising a polypeptide and a physiologically acceptable carrier, the polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

13. A vaccine for the treatment of prostate cancer comprising a polypeptide and a non-specific immune response enhancer, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences

14. The vaccine of claim 13 wherein the non-specific immune response enhancer is an adjuvant.

15. A vaccine for the treatment of prostate cancer comprising a DNA molecule and a non-specific immune response enhancer, the DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

16. The vaccine of claim 15 wherein the non-specific immune response enhancer is an adjuvant.

17. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claims 7 or 12.

18. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of any one of claims 8, 10, 13 or 15.

19. A fusion protein comprising two or more polypeptides according to claim 1.

20. A fusion protein comprising a polypeptide according to claim 1 and a known prostate antigen.

21. A pharmaceutical composition comprising a fusion protein according to any one of claims 19-20 and a physiologically acceptable carrier.

22. A vaccine comprising a fusion protein according to any one of claims 19-20 and a non-specific immune response enhancer.

23. The vaccine of claim 22 wherein the non-specific immune response enhancer is an adjuvant.

24. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claim 21.

25. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of claim 22.